



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 160996

TO: Ruixiang Li
Location: REM/4D75/4C70
Art Unit: 1646
Monday, August 08, 2005

Case Serial Number: 10/626398

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Li,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

THE COMPANY

STIC-Biotech/ChemLib

160986

From: Li, Ruixiang
Sent: Friday, July 29, 2005 4:02 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.10/626,398

Please do a standard search on:

- (i). SEQ ID NO: 10 against commercial amino acid databases.
(ii). SEQ ID NO: 7 and 10 against commercial nucleic acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

RECEIVED
JUL 29 2005
STIC-Biotech/ChemLib
(STIC)

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 8/2/05
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: 1 AA#: 1H1 reverse
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: OS p/000
WWW/Internet: _____
Other(Specify): _____

1880

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 17:26:17 ; Search time 238 Seconds
(without alignments)
8043.881 Million cell updates/sec

Title: US-10-626-398-7

Perfect score: 1170
Sequence: 1 atgttgcgaataacagctac.....accgcctcaatcaccattga 1170

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents NA:*
2: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
3: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
5: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfill1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	57.7	1173	3 US-09-414-010-1	Sequence 1, Appl1
2	675	57.7	1173	4 US-09-812-216-1	Sequence 1, Appl1
3	132.2	11.3	1239	4 US-09-891-053-2	Sequence 2, Appl1
4	132.2	11.3	2700	4 US-09-891-053-5	Sequence 5, Appl1
5	123	10.5	1338	3 US-09-165-543-6	Sequence 6, Appl1
6	123	10.5	1953	4 US-09-891-053-26	Sequence 26, Appl1
7	123	10.5	3244	3 US-09-165-543-4	Sequence 4, Appl1
8	110.2	9.4	1335	2 US-08-985-090-3	Sequence 3, Appl1
9	110.2	9.4	1335	3 US-09-165-543-3	Sequence 3, Appl1
10	110.2	9.4	1335	3 US-09-167-354-6	Sequence 6, Appl1
11	110.2	9.4	1335	3 US-09-642-855-6	Sequence 6, Appl1
12	110.2	9.4	1335	3 US-09-642-514-6	Sequence 6, Appl1
13	110.2	9.4	2050	4 US-09-891-053-21	Sequence 21, Appl1
14	110.2	9.4	2665	4 US-09-949-016-5039	Sequence 5059, Ap
15	110.2	9.4	2689	2 US-08-985-090-1	Sequence 1, Appl1
16	110.2	9.4	2689	3 US-09-165-543-1	Sequence 1, Appl1
17	110.2	9.4	2689	3 US-09-167-354-5	Sequence 5, Appl1
18	110.2	9.4	2689	3 US-09-642-855-5	Sequence 5, Appl1
19	110.2	9.4	2689	3 US-09-642-514-5	Sequence 5, Appl1
20	83.2	7.1	1086	2 US-08-985-090-6	Sequence 6, Appl1
21	83.2	7.1	1086	2 US-09-165-543-33	Sequence 33, Appl1
22	83.2	7.1	2218	2 US-08-985-090-4	Sequence 4, Appl1
23	83.2	7.1	2218	2 US-09-165-543-31	Sequence 31, Appl1
24	73.4	6.3	1386	4 US-09-016-434-1339	Sequence 1339, Ap
25	73.4	6.3	1422	4 US-09-826-509-512	Sequence 512, App
26	73	6.2	1581	1 US-08-313-553-8	Sequence 8, Appl1
27	73	6.2	1581	3 US-08-767-993-8	Sequence 8, Appl1

28	73	6.2	1956	1 US-08-313-553-6	Sequence 6, Appl1
29	73	6.2	1956	3 US-08-767-993-6	Sequence 6, Appl1
30	71.2	6.1	1773	4 US-09-826-509-516	Sequence 516, App
31	71.2	6.1	1913	4 US-09-016-434-1314	Sequence 1314, Ap
32	69.8	6.0	1056	3 US-09-524-162-1	Sequence 1, Appl1
33	69.4	5.9	1401	4 US-09-826-509-514	Sequence 514, App
34	69.4	5.9	2210	4 US-09-016-434-1177	Sequence 1177, Ap
35	69.4	5.9	2210	4 US-10-166-199-1	Sequence 1, Appl1
36	63.8	5.5	1599	4 US-09-826-509-520	Sequence 520, App
37	63.8	5.5	2261	4 US-09-016-434-1176	Sequence 1176, Ap
38	63.2	5.4	601	4 US-09-949-016-177027	Sequence 177027, Ap
39	63.2	5.4	1893	4 US-09-891-053-13	Sequence 13, Appl1
40	63.2	5.4	9293	4 US-09-949-016-16801	Sequence 16801, A
41	55.4	4.7	1101	4 US-09-826-509-432	Sequence 432, App
42	55.4	4.7	1554	2 US-08-031-538-8	Sequence 8, Appl1
43	55.4	4.7	1554	4 US-09-016-434-1301	Sequence 1301, Ap
44	55.4	4.7	1730	1 US-07-817-920-1	Sequence 1, Appl1
45	55.4	4.7	1730	1 US-08-117-006-1	Sequence 1, Appl1

ALIGNMENTS

```
RESULT 1
US-09-414-010-1
; Sequence 1, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Unland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-010-1

Query Match      57.7%; Score 675; DB 3; Length 1173;
Best Local Similarity 74.9%; Pred. No. 2.4e-203;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY      8 CAATATGACGTACATCGCCTTACATCAATTAATTTCTTGACATTTTATGCTT 67
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DB      11 CTAATGACCAATCAATTTATCACTAGACATCGTCTTATGACATTTTATGCTT 70
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QY      68 TCTACTATGCTATTAATGTTAGGCAATGCTGCTATTTAGCTTTATTTAGGACA 127
      |||
DB      71 TACTACTTTTGTATTAATGCTAGGAATGCTTGTCAATTTAGCTTTTGTGTGACA 130
      |||

QY      128 GAATCTTACATCAATCAATTAATTTCTTACTTGGCCATTTGACATCTTTG 187
      |||
DB      131 AAACCTTACATCAATCAATTAATTTCTTACTTGGCCATTTGACATCTTTG 190
      |||

QY      188 TGGGTGATGCTCAATCTCTGTATACATCTTCTGCTGACTTCTGACTTTGGAA 247
      |||
DB      191 TGGGTGATGCTCAATCTCTGTATACATCTTCTGCTGACTTCTGACTTTGGAA 250
      |||

QY      248 AGCAAGCTGTGATTTGGCTATCACTAGCATATTTTATGATCAGATCTGTGATA 307
      |||
DB      251 AGCAATCTGTGATTTGGCTATCACTAGCATATTTTATGATCAGATCTGTGATA 310
      |||

QY      308 AATATGCTCTCATACGATCGATCGTACAGTCAATGCGGTGTGATATAGAG 367
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311 ACATTGCTCATACAGCTATGATGATACCTGCTCAAAAGCTGTGTTATAGAA 370
368 CTCAGCACTCTGGCACTGGAAATGCTACTCAATGAGTGTGCTGTTGATATCTCT 427
371 CTCACATATCTGGGCTTGAAGATTGTTACTGTATGTGTGCTGTTGGGCTGCT 430
428 TCATGACAAATGGCCGATGATGATGATGATGATGATGATGATGATGATGAT 487
431 TCTTAGTGAATGGCCGATGATGATGATGATGATGATGATGATGATGATGAT 490
488 GTGAACCTGGATTTTAAAAAGTGTACTTGTCTCTCTCAATCATATATGGAATCC 547
491 GTGAACCTGGATTTTTCGAATGATGATGATGATGATGATGATGATGATGATG 550
548 TGATCCCATCTTGTAGTGTGCTTATGATGATGATGATGATGATGATGATGATG 607
551 TGATCCCATCTTGTAGTGTGCTTATGATGATGATGATGATGATGATGATGATG 610
608 GAGAGAACTGACAGAGTGTCTGACGACCTGTGATCTCTCTGATCTGTTCCAGAGTG 667
611 GTGATCATCTCAGTAGTGTGCTCAAAAGCTGTGATGATGATGATGATGATGATG 667
668 ACCAGGACATCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727
668 TGTGTGACATCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727
728 AAACAACCTGCTCTCTGTTGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787
728 AAGTTCCTGATCTCTTATGATGATGATGATGATGATGATGATGATGATGATG 787
788 TAAAGCTCTCAAG 847
788 CAAGAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 847
848 ATTCCCTGCTCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
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908 AGTCACTGACATCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 967
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968 CAGTATCTCTCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027
968 CAGTATCTCTCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027
1028 CATTGCTCTCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027
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1148 ACAACCG 1154
1148 ACAACCG 1154

RESULT 2
US-09-812-216-1
Sequence 1, Application US/09812216
Patent No. 6613533
GENERAL INFORMATION:
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Laz, Thomas M.
APPLICANT: Monema, Frederick J. Jr.
APPLICANT: Morse, Kelley L.
APPLICANT: Umland, Shelby P.
APPLICANT: Wang, Suke
TITLE OF INVENTION: Histamine receptor
FILE REFERENCE: CN01069

CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/414,010
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patencin Ver. 2.1
SEQ ID NO 1
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-09-812-216-1
Query Match 57.7%; Score 675; DB 4; Length 1173;
Best Local Similarity 74.9%; Pred. No. 2.4e-203;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;
8 CAAATACAGTACATCCCTTACATCAATTTAAATTTCTTGAATTTTAAATGCT 67
11 CTAATAGCAATCAATTTATCTAGCACTGTTAGCTTATGATGCT 70
68 TACTAGTATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 127
71 TATGATCTTGTCTATATGCTAGAAATGCTTGTGATTTTATGCTTGTGATGATG 130
128 GAAATCTTACAGTACATGATGATGATGATGATGATGATGATGATGATGATG 187
131 AAACCTTACAGTACATGATGATGATGATGATGATGATGATGATGATGATGATG 190
188 TGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 247
191 TGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 250
248 AGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 307
251 AGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 310
308 ATATGCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 367
311 ACATTGCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 370
368 CTCAGCACTCTGGCACTGGAAATGCTACTGATGATGATGATGATGATGATGATG 427
371 CTCACATATCTGGGCTTGAAGATTGTTACTGTATGTGTGCTGTTGGGCTGCT 430
428 TCATGACAAATGGCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 487
431 TCTTAGTGAATGGCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
488 GTGAACCTGGATTTTAAAAAGTGTACTTGTCTCTCTCAATCATATATGGAATCC 547
491 GTGAACCTGGATTTTTCGAATGATGATGATGATGATGATGATGATGATGATGATG 550
548 TGATCCCATCTTGTAGTGTGCTTATGATGATGATGATGATGATGATGATGATGATG 607
551 TGATCCCATCTTGTAGTGTGCTTATGATGATGATGATGATGATGATGATGATGATG 610
608 GAGAGAACTGACAGAGTGTCTGACGACCTGTGATCTCTCTGATCTGTTCCAGAGTG 667
611 GTGATCATCTCAGTAGTGTGCTCAAAAGCTGTGATGATGATGATGATGATGATG 667
668 ACCAGGACATCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727
668 TGTGTGACATCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727
728 AAACAACCTGCTCTCTGTTGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787
728 AAGTTCCTGATCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 787
788 TAAAGCTCTCAAG 847
788 CAAGAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 847
848 ATTCCCTGCTCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907

APPLICANT: Ohta, Masataka
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
FILE REFERENCE: 06501-083001
CURRENT APPLICATION NUMBER: US/09/891,053
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/JP99/07280
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: PCT/JP98/05967
PRIOR FILING DATE: 1998-12-25
PRIOR APPLICATION NUMBER: JP 11/145661
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2700
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: CDS
LOCATION: (351)...(1589)
NAME/KEY: misc feature
LOCATION: (1)...(12700)
OTHER INFORMATION: n = A,T,C or G
US-09-891-053-5

Query Match 11.3%; Score 132.2; DB 4; Length 2700;
Best Local Similarity 48.7%; Pred. No. 6,7e-31;
Matches 523; Conservative 0; Mismatches 528; Indels 24; Gaps 5;

QY 59 TAAATCTTAACTAGCTATTGCTAATATGTTAGGCAATGCTGCTATTGCTTTTA 118
DB 469 TCATGGCCCTGCTCATCGTGGCCACAGTACGCGGCGCTGCTGCTGCTGCTCG 528
QY 119 TTGTGACAGAAATTTAGACATGACATTAATCTTTTCTTACTTGGCATTGAG 178
DB 529 TGGCGGATTCAGGCTCCGACCCAGAACAACTTTCTTGTCTCAACTCCGCACTCG 588
QY 179 ACTCTTTGTGGGTGCAATTGCAATTCCTGTATACATCTTCTCGCTGACTTAC--T 235
DB 589 ACTTCTGTGGGTCTTGTGCAATCCCATTTGATGTAACCTGATGCTGACCGGCTT 648
QY 236 GGAATCTTGAAGACAGCTGTGTATTTTGGCTCATTAAGTACTTCTTTTATGACAG 295
DB 649 GGACCTTGGCGGGGCTCTGCAAGCTGTGCTGTGTAGTACTTACTGTGTGCT 708
QY 296 CATCTGTATTAATTTGCTCATGCTACATGCTGCTACAGCTGCTCAATATGCG 355
DB 709 CTTGGCTTTCACTCTGATCTACTCATAGCTATGACCAATTCCTGTCACTGACGCTG 768
QY 356 TGTGTATAGAGCTGACGCTCTGACCTGCAAAATTTGCTACTGATGTGCTGTTT 415
DB 769 TCTCTTACAGGGCCAGGAGGAGGAGACAGAGACGGGCGGTTCCGAAGATGGACGTGT 828
QY 416 GGATATTTCTCTTCAATGACAAATGGGCGGATGATTTGATTTCAAGCTTTGGCAATA 475
DB 829 GGGTGTCTGCTTCTCTGTATGAGGCTGCTGCTGCTGAGTGGAGATGACCTGTGTG 888
QY 476 GCACTACAG-----AATGGAACCTGATTTTAAAGAGTACTTGTGCTC 523
DB 889 GCACTTCAATCCCGAGGCGCACTCTTGTGAGTGTCTTCTCAACTGGAATCTTCTCA 948
QY 524 TCCCTACATCAATTTAGAAATTCCTGATCCCATCTGTGTAGTGTCTTATTTACGCGCC 583
DB 949 TCAGGGCTCCACCTCGAGTTCTTCAAGGCTTCTCAAGGTTACTTCTTCAACTCA 1008
QY 584 ATATTACTGAGCTGTGGAAGGAGAGAAATGACAGAGGTGCTCAGCCACCTGTAC 643
DB 1009 GATCTTACCTGAACTCAGAGGCGCACCCGCTTGTGCTGATGGGCGCTGAGGCTG 1068
QY 644 TCCCTTGAAGCTTCCAGAGAGTACAGAGACATCCCTGACAGAGACCCCGATTCA 703
DB 1069 GCCCAAGACC---CAACCAATGCCAGCCCTGCGCACTTCCAGCTTCCCCAGCTGC 1124

QY 704 GGGGACTCTGCGACAGCGAAGAAACACTGCTCTTGTGTTACAGACATGACCGGA 763
DB 1125 TGGGGCTGCTGCCAAAGGCGCATGGGCGCATGCGTTGACAGCTTGGCAGCTCC 1184
QY 764 GAAAGAGCATCTCTTGTTCATTAAGGCTTACAGACATGATGCTTCCA 823
DB 1185 TCAAGGGGCACTGAGAGGCGCACTCACTCAAAAGGGGCTCCAGGCCATGACATTTCA 1244
QY 824 AATGGGCTTCTCCCATCAGATTCCTCGGCTCTTACAGAAAGGAGACATATGAC 883
DB 1245 GATTCCTGGAAGGCGCATAGATGCTGTCAGAGACTC--ACCAAGGCTTCCGGC 1302
QY 884 TTTTCAGAGCCAGAAATTTAGCCAAAGTCACTGCGCATCTCTAGACATTTTGGCATTT 943
DB 1303 TGTGCGGGGACAGAGAGGTGCGCAAGTGTGCGCATCATGTGAGCATCTTTGGGCTCT 1362
QY 944 GCTGGCTCCATATTTACTGACTACATTAATCTACTATTTTCTGAAAGAACTTGA 1003
DB 1363 GCTGGCGCCGTACACGCTCTTAATGATCATCGAGCTGTGCTGATGCGCTGATCC 1422
QY 1004 CTAAATCAACTGGTATCATCTGCTTTTGGCTCCAGTGTCAATTCTTTGTTATC 1063
DB 1423 CCGATT--ACTGTACAGAGCTCTTCTGTGCTTGTGGCCAACTGCGCTCAACC 1479
QY 1064 CTTTGTATATCATTTGTGTCAAAACGTTTTCAGAAAGCTTTCCTGAAATACT 1118
DB 1480 CCGTCTCTTACCACTGTGCGACATAGCTTCCGAGAGCCTTTCACCAAGCTCCT 1534

RESULT 5
US-09-165-543-6
Sequence 6, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Gluckeman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1338 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
NAME/KEY: CDS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: NMI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3244 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 778..2112
US-09-165-543-4

Query Match 10.5%; Score 123; DB 3; Length 3244;
Best Local Similarity 54.0%; Pred. No. 6.2e-28;

Matches 305; Conservative 0; Mismatches 245; Indels 15; Gaps 2;

59 TAATGCTTTTACTAGCTATTGCTATTAATGTTAGGCAATGCTGTCATTTTTGA 118
119 TTGCGACAGAAATTTAGACATCGAATTAATTTTCTTAATCTTGCCATTGCG 178
956 TGGCGAATTCGAGCTTCGCGACCCAGAACTTTCTTCTGCTCAACCTCGCATCTCG 1015
179 ACTCTTTGTTGGGTCGCAATTCGCAATTCCTGTCATACCTTCGCTGACTTAC--T 235
1016 ACTTCCTGTTGGGTCCTTCTGCAATCCATTTGATGACCTCATGCTGCTGCGCGCTT 1075
236 GGAATTTCTGGAAGCAAGCTGTGTAATTTGGCTGATTAGTACTGATCTTTTATGTA 295
1076 GGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTGTAAGTACTGATGCTGCT 1135
296 CATCTGTGTAATTAATTTGCTCATCAGTACGATGCGTACACAGTCTTCAATGCG 355
1136 CCTCGGCTTCAACATCGTACTCAGTACGATGACCGAATTCCTGTCAGTCACTCGAGCTG 1195
356 TGTGATATAGAGCTCAGCACTCTGCGACCTGGAAATTTGCTACTGATGCTGCTGTTT 415
1196 TCTCTTACAGGGCCAGAGAGGGGACAGAGAGCGGCGTTTCGAAAGATGGACGCTGT 1255
416 GGAATTTCTCTTATGACAAATGSGCGAGATTTCTGATTTCACTCTTGGCAGAA 475
1256 GGGTGTCTGCTCTCTGCTGTAATGGGCTGCGCATCTGAGTTGGAGATCACTGTGCTG 1315
476 GCACTAGAG-----AATGTAACCTGGAATTTTAAAGAGGTAATTTGCTC 523
1316 GAGTTTCAATCCCGAGGGCCACTGTAATGCTGAGTTCTTCAACAGTGAATTTTCA 1375
524 TCCCTACATCAATTAATGGAATTCCTGATCCCATCTTGTAGTTGCTTATTTCA 583
1376 TCAAGGCTTCAACCTCGAGTTCTTCAAGGCTTCTCAAGCTTCACTTCTTCACTCA 1435
584 AATATTACTGAGCTGTGGAAGCG 608
1436 GCATCTACCTGAAATCCAGAGCG 1460

RESULT 8

US-08-985-090-3
Sequence 3, Application US/08985090
Patent No. 5885893
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silverl
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: NMI-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1335
US-08-985-090-3

Query Match 9.4%; Score 110.2; DB 2; Length 1335;
Best Local Similarity 52.6%; Pred. No. 4.1e-24;

Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;

59 TAATGCTTTTACTAGCTATTGCTATTAATGTTAGGCAATGCTGTCATTTTTGA 118
119 TCATGGCGCTCTCATCTGCGCAACGCTGCGCAACGCTGTGTCATGCTGCGCTTCG 178
119 TTGCGACAGAAATTTAGACATCGAATTAATTTTCTTAATCTTGCCATTGCG 178
179 TGGCGAATTCGAGCTTCGCGACCCAGAACTTTCTTCTGCTCAACCTCGCATCTCG 238
179 TGGCGAATTCGAGCTTCGCGACCCAGAACTTTCTTCTGCTCAACCTCGCATCTCG 238
179 ACTCTTTGTTGGGTCGCAATTCGCAATTCCTGTCATACCTTCGCTGACTTAC--T 235
239 ACTTCCTGTTGGGCTCTTCTGCAATCCATTTGATGACCTCATGCTGCTGACGCGCT 298
236 GGAATTTCTGGAAGCAAGCTGTGTAATTTGGCTGATTAATGATGATCTTTTATGTA 295
239 GGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTGTAAGTACTGATGCTGCTGCTC 358
296 CATCTGTGTAATTAATTTGCTCATCAGTACGATGCGTACACAGTCTTCAATGCG 355
359 CTTCTGCTTCAACATCGTACTCAGTACGATGACCGTCTCTGCGGTCAACCGAGCG 418
356 TGTGATATAGAGCTCAGCACTCTGCGACCTGGAAATTTGCTACTGATGCTGCTGTTT 415
419 TCTCATACGGGGCCAGAGAGGGTACACGCGGCGGAGTGGAGAAATGCTGCTGCTGT 478
416 GGAATTTCTCTTATGACAAATGSGCGAGATTTCTGATTTCACTCTTGGCAGAA 475

DB 479 GGGTGTGGGCTTCCTGCTGTACGACCAAGCCATCTGAGTACCTGCGGGG 538
QY 476 GCACCTAC-----AGAAATGGAACCTGGAATTTTAAAAAGTGTACTTGTCTC 523
DB 539 GCAGCTTCATCCCGAGGCGCACTGTATGCCAGATCTTCTCAACTGTGTACTTCTCA 598
QY 524 TCCCTACATCATTAATTTGAATTCCTGATCCCATCTTGTAGTGTATTTGAGCGGCC 583
DB 599 TCAGGCTTCACCGCTGAGATTTTTCACGCTTCTCAGCGTACCTTTTAACTCA 658
QY 584 AATATTACTGAGCCTGTGGACCG 608
DB 659 GCATCTACCTGAACATCCAGAGCG 683

RESULT 9
US-09-165-543-3
; Sequence 3, Application US/09165543
; Patent No. 6093545

GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:

ATTORNEY/AGENT INFORMATION:

; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ. ID NO: 3:

SEQUENCE CHARACTERISTICS:

; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

; NAME/KEY: CDS
; LOCATION: 1..1335
US-09-165-543-3

Query Match 9.4%; Score 110.2; DB 3; Length 1335;
Best Local Similarity 52.6%; Pred. No. 4.1e-24;
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;

QY 59 TAATGCTTTACTAGCTATATGTTAGCAATGTCGTGCTATTTAGCTTTTA 118
DB 119 TCATGGCGCTGCTCATCTGTCGACCGTGTGGCAACGCGCTGTCATCTGCTTCG 178
QY 119 TTGTGACAGAAATCTTGAATGCAATGCAATTAATTTTCTTAACCTTGCCATTCGAG 178
DB 179 TGCGCAGCTGAGACCTCCGACCAAGAACTTTCTTCGTCACCTGCGCATCTCCG 238

QY 179 ACTTCTTGGGAGTGAATTTGCAATTCCTGTGATACATCTTCTGCTGAC---TTACT 235
DB 239 ACTTCTCTGTCGCGGCTTCTGCTGATCCACTGTATGTACCTTACCTGTACAGCGCGCT 298
QY 236 GGAATTTCTGGAAGCAAGCTTGTATTTTGGCTCATTAAGTATCTTTTATGATACAG 295
DB 299 GGAATTTCTGGAAGCAAGCTTGTATTTTGGCTCATTAAGTATCTTTTATGATACAG 358
QY 296 CATCTGTATTAATTAATTTGCTTCATCATGATGATGCTTACAGTCAAGTCTCAATGCGC 355
DB 359 CCTCTGCTTCAACATCTGCTCATGATGATGATGATGATGATGATGATGATGATGATGAT 418
QY 356 TGTGTATGAGCTCAGCACTGCGACCTGGAATTTGCTACTTCAAGATGATGATGATGAT 415
DB 419 TCTCATACCGGCT 478
QY 416 GGAATTTCTTCTTCATGACAAATGAGCGCGATGATGATGATGATGATGATGATGATGATGAT 475
DB 479 GGGTGTGGGCTTCCTGCTGTACGACCAAGCCATCTGAGCTGGAGTACTGTGCGGGG 538
QY 476 GCACCTAC-----AGAAATGGAACCTGGAATTTTAAAAAGTGTACTTGTCTC 523
DB 539 GCAGCTTCATCCCGAGGCGCACTGTATGCCAGATCTTCTCAACTGTGTACTTCTCA 598
QY 524 TCCCTACATCATTAATTTGAATTCCTGATCCCATCTTGTAGTGTATTTGAGCGGCC 583
DB 599 TCAGGCTTCACCGCTGAGATTTTTCACGCTTCTCAGCGTACCTTTTAACTCA 658
QY 584 AATATTACTGAGCCTGTGGACCG 608
DB 659 GCATCTACCTGAACATCCAGAGCG 683

RESULT 10

US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 6136559

GENERAL INFORMATION:

; APPLICANT: Lovendberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree

; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3

FILE REFERENCE: SUBTYPE

; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ. ID NOS: 8

SOFTWARE: PatentIn Ver. 2.0

SEQ. ID NO 6

LENGTH: 1335

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: cDNA
US-09-167-354-6

Query Match 9.4%; Score 110.2; DB 3; Length 1335;
Best Local Similarity 52.6%; Pred. No. 4.1e-24;
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;

QY 59 TAATGCTTTACTAGCTATATGTTAGCAATGTCGTGCTATTTAGCTTTTA 118
DB 119 TCATGGCGCTGCTCATCTGTCGACCGTGTGGCAACGCGCTGTCATCTGCTTCG 178
QY 119 TTGTGACAGAAATCTTGAATGCAATGCAATTAATTTTCTTAACCTTGCCATTCGAG 178
DB 179 TGCGCAGCTGAGACCTCCGACCAAGAACTTTCTTCGTCACCTGCGCATCTCCG 238
QY 179 ACTTCTTGGGAGTGAATTTGCAATTCCTGTGATACCTTCTGCTGAC---TTACT 235
DB 239 ACTTCTCTGTCGCGGCTTCTGCTGATCCACTGTATGTACCTTACCTGTACAGCGCGCT 298

QY 236 CATCTGTATATAATTTCTCATCATGATGCTACAGTCTCAATGCGG 355
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Db 359 CCTCTGCTTCAACATCGTCTCATAGCTACGACCGCTTCTGTGGTACCCGACGG 418
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QY 356 TGTGTATAGAGCTCAGACTCTGGACCTGGAAAATTTCTACTCATGATGTGGCTGTT 415
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Db 419 TCTCATACGGGGCCCGCAGAGGAGACCGGGGGGACATGGGAAAGATGTGCTGTGT 478
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QY 416 GGATATTCCTTCATGACAAATGGCCGATGATTTGATTTCAAGCTCTGGCAGAAAT 475
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Db 479 GGGTGTGGCTTCTCTGTGTAGAGACGACCATCTGTAGCTGGAGTACTGTCCGGGG 538
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QY 476 GCACTAC-----AGAAATGAACTGTGATTTTAAAAAGTGTACTTGTCTC 523
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Db 539 GAGCTCCATCCCCGAGGGGCACTGTATGCGGAGTTCTTCAACATGTGACTTCTCTA 598
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QY 524 TCCCTACATCATTTATTTGAATTCCTGATCCCATCTTGTAGTTGCTTATTTCAAGGCC 583
| | | | |
Db 599 TCACGGCTTCCACCCCTGGAGTTCTTTACGCCCTTCTCAGCGCTCACTTTAACTCTCA 658
| | | | |
QY 584 ATATTACTGAGCGCTGTGGAAGCG 608
| | | | |
Db 659 GCATCTACCTGAACATCCAGAGCGG 683
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RESULT 13
US-09-891-053-21
; Sequence 21, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraoku
; APPLICANT: Takimura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1998-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 2050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271)...(1629)
US-09-891-053-21

Query Match 9.4%; Score 110.2; DB 4; Length 2050;
Best Local Similarity 52.6%; Pred. No. 5.4e-24;
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;

QY 59 TATGCTTTACTAGTATTTGCTATTAATTTAGCAATGTCGTGATTTAGCTTTTA 118
| | | | |
Db 389 TATGCGCTGCTCATGCTGCGACCGTGTGGCAACGGGCTGTGATGCTGCTTGG 448
| | | | |
QY 119 TGTGACAGAAATCTTACATGCAAGTAATTTACTTTTCTTAATCTGGCATTGCA 178
| | | | |
Db 449 TGGCCGACTGAGCGCTCGACCCAGAACAACTTCTCTGCTCAACCTGCGCATCTCG 508
| | | | |
QY 179 ACTTCTTTGGGTGCAATTTGCAATTCCTCTGACACTTCTGCTGAC---TTACT 235
| | | | |

Db 509 ACTTCTCTGCGCGCTTCTGATCCCATGTATGTACCTTACGTGACAGCGCGCT 568
| | | | |
QY 236 GGAATTTGAGAAAGCAAGTTGTGATTTTGGCTCAATTACTATCTTTATATAGAG 295
| | | | |
Db 569 GGAATTTGAGAAAGCAAGTTGTGATTTTGGCTCAATTACTATCTTTATATAGAG 628
| | | | |
QY 296 CATCTGTATATAATTTCTCATCATGATGCTACAGTCTCAATGCGG 355
| | | | |
Db 629 CCTCTGCTTCAACATCGTCTCATAGCTACGACCGCTTCTGTGGTACCCGACGG 688
| | | | |
QY 356 TGTGTATAGAGCTCAGACTCTGGACCTGGAAAATTTCTACTCATGATGTGGCTGTT 415
| | | | |
Db 689 TCTCATACGGGGCCCGCAGAGGAGACCGGGGGGACATGGGAAAGATGTGCTGTGT 748
| | | | |
QY 416 GGATATTCCTTCATGACAAATGGCCGATGATTTGATTTCAAGCTCTGGCAGAAAT 475
| | | | |
Db 749 GGGTGTGGCTTCTCTGTGTAGAGACGACCATCTGTAGCTGGAGTACTGTCCGGGG 808
| | | | |
QY 476 GCACTAC-----AGAAATGAACTGTGATTTTAAAAAGTGTACTTGTCTC 523
| | | | |
Db 809 GAGCTCCATCCCCGAGGGGCACTGTATGCGGAGTTCTTCAACATGTGACTTCTCTA 868
| | | | |
QY 524 TCCCTACATCATTTATTTGAATTCCTGATCCCATCTTGTAGTTGCTTATTTCAAGGCC 583
| | | | |
Db 869 TCACGGCTTCCACCCCTGGAGTTCTTTACGCCCTTCTCAGCGCTCACTTTAACTCTCA 928
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QY 584 ATATTACTGAGCGCTGTGGAAGCG 608
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Db 929 GCATCTACCTGAACATCCAGAGCGG 953
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RESULT 14
US-09-949-016-5059
; Sequence 5059, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5059
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5059

Query Match 9.4%; Score 110.2; DB 4; Length 2665;
Best Local Similarity 52.6%; Pred. No. 6.3e-24;
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;

QY 59 TATGCTTTACTAGTATTTGCTATTAATTTAGCAATGTCGTGATTTAGCTTTTA 118
| | | | |
Db 410 TATGCGCTGCTCATGCTGCGACCGTGTGGCAACGGGCTGTGATGCTGCTTGG 469
| | | | |
QY 119 TGTGACAGAAATCTTACATGCAAGTAATTTACTTTTCTTAATCTGGCATTGCA 178
| | | | |
Db 470 TGGCCGACTGAGCGCTCGACCCAGAACAACTTCTCTGCTCAACCTGCGCATCTCG 529
| | | | |
QY 179 ACTTCTTTGGGTGCAATTTGCAATTCCTCTGACACTTCTGCTGAC---TTACT 235
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Db 530 ACTTCTCTGCGCGCTTCTGATCCCATGTATGTACCTTACGTGACAGCGCGCT 589
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QY 236 GGACTTTGGAAGCAAGCTGTGATTTTGGCTCATTACTGACTATCTTTTATGTACAG 295
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Db 590 GGACCTTGCGCCGGGCGCTCTGCAAGCTGTGCTAGTGTGACTACCTGCTGCACCT 649
QY 236 CATCTGTATATATATTTGCTTCATCAGCTAGATCGCTACCAAGTCAGTCAAAATGCCG 355
    |||||
Db 650 CCTGTGCTTCAACATCGTGTCTATCAGTACGACCGCTCTGTGTGGTCAACCGACGG 709
QY 356 TGTGTATAGAGCTGCACTGTGCACTGGAATAATTGCTACTGATGAGTGTGCTGTTT 415
    |||||
Db 710 TCTCATACCGGGCCGACGAGGTGACACGGCGGGCAGTGGGAAAGTGTGCTGTCT 769
QY 416 GGAATTTCTCTTATGACAAATGGCGCATATTTGATTTCAACTCTTGGCAGAATA 475
    |||||
Db 770 GGGTCTGGCTTCTCTGTGTGACGACCGACCTCTGAGTGGAGTACCTGTCCGGGG 829
QY 476 GCACTAC-----AGATGGAACCTGSAATTTTAAAAAGGTACTTTGCTC 523
    |||||
Db 830 GCACTTCATCCCGAGGGCCACTGTATGCCGAGTTCTTCAACATGTGATCTTCTCA 889
QY 524 TCCCTACATCATTTATTTGGAATTCCTGATCCCATCTTTGTTAGTGTCTTATTTCAAGCGCC 583
    |||||
Db 890 TCAGGCTTCCACCGCTGGAGTTCTTTAGCGCTCTCTCAAGCTTCTTTAAGCTCA 949
QY 584 ATATTACTGAGCGCTGTGGAAGCG 608
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Db 950 GCATCTACCTGAACATCCAGAGCG 974
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RESULT 15

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US-08-985-090-1
; Sequence 1, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodear1
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silver1
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-08-985-090-1

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Query Match          9.4%; Score 110.2; DB 2; Length 2689;
Best Local Similarity 52.6%; Pred. No. 6.4e-24;
Matches 297; Conservative 0; Mismatches 255; Indels 15; Gaps 2;

QY 59 TAAATCTTTACTAGCTATTTGCTATATGTTAGCAATGTGTGCTATTTTACTTTTAA 118
    |||||
Db 409 TCATGGCGCTCTCATCGTGGCCACGCTGTGGGCAACGGCTGTGATGCTCGCTTCG 468
QY 119 TTGTGACAGAAATTTAGATAGTAAATTAATTTTCTTTTCTTAATCTGGCAATTGAC 178
    |||||
Db 469 TGGCGAATCGAGCTTCGCCACCAAGAAACATTTCTCTGCTCAACCTCGCATCTCCG 528
QY 179 ACTTCTTGTGGGTGCAATTTGCAATTCCTCTGTACATACCTTCTCGCTGAC---TACT 235
    |||||
Db 529 ACTTCTGTGGGGCTTCTGTGCAATCCACATGTATGTACCTAGCGTGTGACAGGCCGT 588
QY 236 GGACTTTGGAAGCAAGCTGTGTATTTTGGCTCATTAAGTACTATCTTTTATGTACAG 295
    |||||
Db 589 GGACCTTGGCGGGGCTCTGTGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 648
QY 236 CATCTGTATATATATTTGCTTCATCAGCTAGATCGCTACCAAGTCAGTCAAAATGCCG 355
    |||||
Db 649 CCTGTGCTTCAACATGTGTCTCATCAGCTACGACCGCTTCTGTGCTGATCCGACGCG 708
QY 356 TGTGTATAGAGCTGACACTGTGGCACTGTGAAATTTGCTACTGAGATGTGTGCTGTTT 415
    |||||
Db 709 TCTCATACCGGGCCGACGAGGTGTACACGGCGGGCAGTGGGAAAGTGTGTGTGTGT 768
QY 416 GGAATTTCTCTTATGACAAATGGCGCATATTTGATTTCAACTCTTGGCAGAATA 475
    |||||
Db 769 GGGTGTGGCTTCTCTGTGTGACGACCGCATCTTCAAGTGGAGTACCTGTCCGGGG 828
QY 476 GCACTAC-----AGATGGAACCTGSAATTTTAAAAAGGTACTTTGCTC 523
    |||||
Db 829 GCACTTCATCCCGAGGGCCACTGTATGCCGAGTTCTTCAACATGTGATCTTCTCA 888
QY 524 TCCCTACATCATTTATTTGGAATTCCTGATCCCATCTTTGTTAGTGTCTTATTTCAAGCGCC 583
    |||||
Db 889 TCAGGCTTCCACCGCTGGAGTTCTTTAGCGCTTCTCTCAAGCTTCTTTAAGCTCA 948
QY 584 ATATTACTGAGCGCTGTGGAAGCG 608
    |||||
Db 949 GCATCTACCTGAACATCCAGAGCG 973
    |||||

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Search completed: August 5, 2005, 20:19:22
 Job time : 241 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 15:18:45 ; Search time 5069 Seconds
(without alignments)
1184.179 Million cell updates/sec

Title: US-10-626-398-7

Perfect score: 1170
Sequence: 1 atcgttgscataacacagctac.....accgctcacaatccacttga 1170

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1170	100.0	1451	10	AF358858 Cavia por
2	675	57.7	1173	6	AR142850 Sequence
3	675	57.7	1173	6	AR391860 Sequence
4	675	57.7	1173	6	AX109119 Sequence
5	675	57.7	1173	6	AX139113 Sequence
6	675	57.7	1173	6	AX301763 Sequence
7	675	57.7	1173	6	BD015847 Novel pol
8	675	57.7	1173	9	AF307973 Homo sapi
9	675	57.7	1173	9	AF325356 Homo sapi
10	675	57.7	1173	9	AF329449 Homo sapi
11	675	57.7	1173	9	AY008280 Homo sapi
12	675	57.7	1173	9	AY136745 Homo sapi
13	675	57.7	1173	9	HS4298292 Homo sapi
14	675	57.7	1266	6	AX376577 Sequence
15	675	57.7	1300	6	AX301229 Sequence
16	675	57.7	1312	6	BD095598 Novel gua
17	675	57.7	1312	9	AB045370 Homo sapi
18	675	57.7	1316	9	BC069136 Homo sapi
19	675	57.7	3689	6	AX549343 Sequence

20	675	57.7	3689	9	AF312230 Homo sapi
21	671.8	57.4	1227	6	BD097512 Novel gua
22	671.8	57.4	1265	9	AB044934 Homo sapi
23	636.8	54.4	1291	4	AB053300 Sus scrofa
24	616.8	52.7	1533	10	AF358860 Rattus no
25	613	52.4	1538	10	AF358859 Mus muscu
26	444.8	38.0	140555	9	AC007922 Homo sapi
27	444.8	38.0	166206	2	AC009668 Homo sapi
28	444.8	38.0	167296	2	AP002507 Homo sapi
29	444.8	38.0	169144	9	AC090244 Homo sapi
30	444.8	38.0	184938	2	AP002476 Homo sapi
31	444.8	38.0	193779	2	AP001327 Homo sapi
32	400	34.2	236694	2	AC118386 Rattus no
33	395.4	33.8	199837	10	AC131672 Mus muscu
34	285.2	24.4	528	9	AY561469 Pan trogl
35	283	24.2	522	9	AY561470 Gorilla g
36	270	23.1	1326	6	AX451922 Sequence
37	269	23.0	429	6	CQ727333 Sequence
38	155.4	13.3	223	6	AX775381 Sequence
39	138	11.8	721	6	AX230341 Sequence
40	132.2	11.3	1239	6	E39806 Novel guano
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43	132.2	11.3	2700	6	E39809 Novel guano
44	132.2	11.3	2700	6	AR559673 Sequence
45	126	10.8	1249	10	AF267538 Cavia por

ALIGNMENTS

RESULT 1
LOCUS AF358858 1451 bp mRNA linear ROD 02-SEP-2001
DEFINITION Cavia porcellus histamine H4 receptor mRNA, complete cds.
ACCESSION AF358858
VERSION AF358858.1 GI:15420532

KEYWORDS
SOURCE
ORGANISM
Cavia porcellus (domestic guinea pig)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.

REFERENCE
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
TITLE Comparison of human, mouse, rat, and guinea pig histamine H4
receptor suggests substantial species variation

Query Match 100.0%; Score 1170; DB 10; Length 1451;
Best Local Similarity 100.0%; Pred. No. 3.9e-284;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGCAATTAACAGTACATCGCTTAACATCAATTAATTTCTTGACATTTT 60
DB 101 ATGTGGCAATTAACAGTACATCGCTTAACATCAATTAATTTCTTGACATTTT 160
QY 61 ATGTCTTACTAGCTATTGCTTAATAGTGAAGCAATGCTGATCAATTTAGCTTTAT 120
DB 161 ATGTCTTACTAGCTATTGCTTAATAGTGAAGCAATGCTGATCAATTTAGCTTTAT 220
QY 121 GTGACAGAAATCTTAGACATCGAAGTAATCTTTTCTTAACCTTGCCATTCGAC 180
DB 221 GTGACAGAAATCTTAGACATCGAAGTAATCTTTTCTTAACCTTGCCATTCGAC 280
QY 181 TTCTTTGGGGGCAATTGCAATTCCTCTGACATACCTCTCTGCTGACTTACAGACT 240
DB 281 TTCTTTGGGGGCAATTGCAATTCCTCTGACATACCTCTCTGCTGACTTACAGACT 340
QY 241 TCTGAAAGCAAGCTGTGTATTTTGGCTCATTTACTGATCTATTATATGACAGATCT 300
DB 341 TCTGAAAGCAAGCTGTGTATTTTGGCTCATTTACTGATCTATTATATGACAGATCT 400
QY 301 GTGTATATATTTGCTCTCATACGTAAGATCCCTACAGTCAAGTCAATCCCTGTG 360
DB 401 GTGTATATATTTGCTCTCATACGTAAGATCCCTACAGTCAAGTCAATCCCTGTG 460
QY 361 TATAGAGCTCAGACCTGCGCACTCGGAAATTTGCTACTCAGATGCTGCTTTGGAA 420
DB 461 TATAGAGCTCAGACCTGCGCACTCGGAAATTTGCTACTCAGATGCTGCTTTGGAA 520
QY 421 TTCTCTTCATGACAAATGGCCGATGATTTGATTTGACATCTTTGGCAATAGACT 480
DB 521 TTCTCTTCATGACAAATGGCCGATGATTTGATTTGACATCTTTGGCAATAGACT 580
QY 481 ACAGAAATGGAACCTGGATTTTAAAAAGTGATCTTCTCTCTCATCATATTATG 540
DB 581 ACAGAAATGGAACCTGGATTTTAAAAAGTGATCTTCTCTCTCATCATATTATG 640
QY 541 GAATTCCTGATCCCATCTGTGTTAGTGTGTTATTTGAGGCGCATTTACGAGCCG 600
DB 641 GAATTCCTGATCCCATCTGTGTTAGTGTGTTATTTGAGGCGCATTTACGAGCCG 700
QY 601 TGGAAAGCAGAGAACTGAGCAGTGTCTCAGCAACCTGTACTCCCTCTGACTTTCC 660
DB 701 TGGAAAGCAGAGAACTGAGCAGTGTCTCAGCAACCTGTACTCCCTCTGACTTTCC 760
QY 661 AGCAGTGAACGAGACATCTCTGACAGACGACCCCGATTTCAAGGGCGACTTGCACGA 720
DB 761 AGCAGTGAACGAGACATCTCTGACAGACGACCCCGATTTCAAGGGCGACTTGCACGA 820
QY 721 CGGAAAGAAACAACCTGCTCTGTGTTAGCAAGTCAAGGACGAGAAAGCATGCTCTG 780
DB 821 CGGAAAGAAACAACCTGCTCTGTGTTAGCAAGTCAAGGACGAGAAAGCATGCTCTG 880
QY 781 TTTTCCATTAAGAGCTTACAGAAACAGCAATGTGATGCTTCCAAATGGGCTTCTCTCC 840
DB 881 TTTTCCATTAAGAGCTTACAGAAACAGCAATGTGATGCTTCCAAATGGGCTTCTCTCC 940
QY 841 CACTCAGATTCCTGCTCTTACAGAAAGGAAATATGAACTTTTACAGCCAGGAAA 900
DB 941 CACTCAGATTCCTGCTCTTACAGAAAGGAAATATGAACTTTTACAGCCAGGAAA 1000
QY 901 TTAGCCAACTCACTGGCCATCTTAGAGAGCTTTGCAATTTGCGGGCTCATATTA 960
DB 1001 TTAGCCAACTCACTGGCCATCTTAGAGAGCTTTGCAATTTGCGGGCTCATATTA 1060
QY 961 CTGACTACAGTTATCTACTCATTTTCTGAAAGGAACTTGAATCAACCTGTATC 1020
DB 1061 CTGACTACAGTTATCTACTCATTTTCTGAAAGGAACTTGAATCAACCTGTATC 1120
QY 1021 CACTGCTCTTTGGCTCAGAGGCTTCAATTCCTTTTAAATCCCTTTTGTATCCATTG 1080

DB 1121 CATACTGCTTTTGGCTCAGAGGTTCAATTCCTTTGTTAATCCCTTTTGTATCCATTG 1180
QY 1081 TGTCCAAACGTTTTCAAGAGCTTCTGAAAATACTTCCGTTGAGAAAGCAATCCACG 1140
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DB 1241 CCACCACAAACCGCTCAATATCCACTTGA 1270

RESULT 2
ARI42850 1173 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 1 from patent US 6204017.
DEFINITION ARI42850
ACCESSION ARI42850
VERSION ARI42850.1 GI:15104136
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 1173)
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monema,F.J., Morse,K.L.,
LOCUS Umland,S.P. and Wang,S.
TITLE Polynucleotide encoding a histamine receptor
JOURNAL Patent: US 6204017-A 1 20-MAR-2001;
FEATURES
location/Qualifiers
1..1173
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 57.7%; Score 675; DB 6; Length 1173;
Best Local Similarity 74.9%; Pred. No. 2.7e-159;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAATTAACAGTACATTCGCTTAACATCAATTAATTTCTTGACATTTTAAATGCTT 67
DB 11 CTAATAGCAATCAATTTATTCATAGACATCGTGTACTTACATTTTATGTCCT 70
QY 68 TACTAGCTATTGCTATTAATGTTAGCAATGCTGCTGATCTTTAGCTTTATTTGAGACA 127
DB 71 TAGTAGCTTTGCTTAATATGCTAGGAAATGCTTGTGATCTTTTGTGTTGAGACA 130
QY 128 GAATCTTAGACATGAAGTATTAATCTTTTCTTAACCTGGCATTGACACTTCTTG 187
DB 131 AAACCTTAGACATGAAGTATTAATCTTTTCTTAACCTGGCATTGACACTTCTTG 190
QY 188 TGGGTGCAATGCAATTCCTCTGTACATACCTTCTGCTGACTTACTGACTTCTGAA 247
DB 191 TGGGTGATCTCAATTCCTTTGTATATCCCTCACACGCTGTTGAAATGGATTTGGAA 250
QY 248 AGCAAGCTTGATTTTGGGCTCATTTACTGACTATCTTTTATGTACAGATCTGTGATA 307
DB 251 AGCAAGCTTGATTTTGGGCTCATTTACTGACTATCTTTTATGTACAGATCTGTGATA 310
QY 308 ATATTGCTCTCATCAGCTACGATGCTACAGATGCTCAATATGCGGTGTGATAAG 367
DB 311 ACATTGCTCTCATCAGCTATGATGATACCTGTCTCAATGTCTGTCTTATAGAA 370
QY 368 CTCAGACTTGGCACTGGAAAATTTGTAATCTAGATGAGTGTGCTTTGATATTTCTCT 427
DB 371 CTCAGACTTGGGCTGTGAAAGATTTGTAATCTGTAGTGTGCGGTGAGTGTGCTCT 430
QY 428 TCATGACAAATGGGCGCATGATCTTGATTTTACAGACTCTTTGAGAAATAGACATAGAT 487
DB 431 TCTTAGTGAATGGGCGCAATGATTTAGATTTGAGATCTTTGAGAAATAGATAGAT 490
QY 488 GTGAACCTGGATTTTAAAAAGTGTAATTTGCTCTCCCTCATCATATTTGGAATTC 547
DB 491 GTGAACCTGGATTTTTCGGAATGTACATCTTGGCATCAATCATATTTCTTGAATTCG 550

QY 548 TGAATCCCATCTTGTAGTTGCTTAATTTTCAGCCCATATTTTACTGAGCCTGTGAGC 607
DB 551 TGAATCCCATCTTGTAGTTGCTTAATTTTCAGCCCATATTTTACTGAGCCTGTGAGC 610
QY 608 GAGAGAAATGAGCAGGTGCTTCAAGCCCTGTACTCCCTCTGACTCTTTCAGAGTGTG 667
DB 611 GTGATCATCTCACTAGAGTGCCTGAGCCATCTGAGCTGAGCTGTCTCTTCCAAACA --- 667
QY 668 ACCAGGACATCTCTGACAGCAGAGCCCATTTCAAGGGGAGACTGTCCGACGACGAGAA 727
DB 668 TCTGTGACACTATTCAGAGTGAAGTATCTTCAAGAGAGATCTTCTTGTGATCAGAG 727
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DB 728 AATCTCTGATCTCTTCAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787
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DB 788 CAAGAACCAAGATGATAGCAATATCAATGCTTCCAAATGGGCTTCTCTCCAAATGAG 847
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DB 848 ATTCTGTAGCTCTTTCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
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DB 1088 AAGCTTTTCAAGAGGCTTCTCTGAAATACTCTCTGTGAGAGAGAGAGAGAGAGAGAG 1147
QY 1148 ACAACCG 1154
DB 1148 AACACAG 1154

RESULT 3
AR391860 1173 bp DNA linear PAT 18-DEC-2003
LOCUS AR391860 Sequence 1 from patent US 6613533.
DEFINITION AR391860
ACCESSION AR391860
VERSION AR391860.1 GI:40115588
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Behar, J. K., Hedrick, J. A., Laz, T. M., Monema, F. J., Morse, K. L.,
Umland, S. P. and Wang, S.
TITLE Histamine receptor
JOURNAL Patent: US 6613533-A 1 02-SEP-2003;
FEATURES
location/Qualifiers
1..1173
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 57.7%; Score 675; DB 6; Length 1173;
Best Local Similarity 74.9%; Pred. No. 2,7e-159;
Matches 855; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATAACAGTACATGCTTAAACATCAATTAATTTCTTGTGACATTTTATGTCCT 67
DB 11 CTAATAGCAATCAATTTATCACTAGCACTGCTTACTTGTAGCATTTTATGTCCT 70

QY 68 TACTAGCTATGCTATATGTTAGGCAATGCGNGCATTTTGTAGCTTTTATTTGAGACA 127
DB 71 TACTAGCTATGCTATATGTTAGGCAATGCGNGCATTTTGTAGCTTTTATTTGAGACA 130
QY 128 GAATCTTACATCAAGATTAATTTTCTTAACTTGTGAGGCAATTTGAGACTTCTTTG 187
DB 131 AAAACCTTACATCAAGATTAATTTTCTTAACTTGTGAGGCAATTTGAGACTTCTTTG 190
QY 188 TGGTGCAATTTGCAATTTCTTGTATACATCTTCTGAGTCTTGTGAGACTTGTGAGAA 247
DB 191 TGGTGCAATTTGCAATTTCTTGTATACATCTTCTGAGTCTTGTGAGACTTGTGAGAA 250
QY 248 AGCAGCTGTGTATTTTGGCTTACTTACATCTTCTTGTATACATCTTGTATACATCT 307
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QY 1148 ACAACCG 1154
DB 1148 AACACAG 1154

RESULT 4
LOCUS AX109119 1173 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 1 from Patent WO0125432.
ACCESSION AX109119
VERSION AX109119.1 GI:13924093
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 Behan, J. X., Hedrick, J. A., Laz, T. M., Monema, F. J., Morse, K. L.,
AUTHORS Umland, S. and Wang, S.
TITLE Histamine receptor
JOURNAL Patent: WO 0125432-A 1 12-APR-2001,
SHERING CORPORATION (US)
FEATURES
source location/Qualifiers
1..1173
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 57.7%; Score 675; DB 6; Length 1173;
Best Local Similarity 74.9%; Pred. No. 2.7e-159;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAATTAACAGTACATCCGCTTAACATCAATTAATTTCTTGAATTTTAATGCTT 67
DB 11 CTAATAGCAATTCATTTATCATCAGACATCGTGTAATTTAGCATTTTATGTCCT 70
QY 68 TACTAGCTATTGCTTAATAGTTAGGCAATGCTGTCATTTTATTTATTTAGTACA 127
DB 71 TAGTAGCTTTTCTTAATAGTAGGAAATGCTTTGTCATTTTATTTAGCTTTTGTGGAGCA 130
QY 128 GAAATCTTAGACATGCAATTAATTTCTTTTCTTAATCTGGCCATTCGACTCTTTG 187
DB 131 AAAACCTTAGACATGCAATTAATTTCTTTTCTTAATCTGGCCATTCGACTCTTTG 190
QY 188 TGGGTGCAATTCCTCTGTACATACCTTCCGCTGACTTACTAGGACTTGTGGA 247
DB 191 TGGGTGTATCTTCATTTCTTTGTACATCTCTCACACGCTGTTCGATGGGATTTTGGAA 250
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DB 251 AGGAATCTGTATTTTGGCTCATTTACTGACTATCTTTATGTACAGCATCTGTATATA 310
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DB 491 GTGAACCTGGATTTTGGAAATGTTATCTTGGCCATCAATCATTTCTTGGAAATTCG 550
QY 548 TGAATCCCATCTTGTAGTTGCTTATTTAGGCGCCATATTTACTGGAGCTGTGGAAGC 607
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QY 608 GAGAGAACTGAGCAGTGTCTCAGCCACCTGTACTCTCCCTCTGTACTCTTCCACAGTG 667
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QY 788 TAAGACCTTAAGAAAGACAGATGTATGCTTCCAAATAGGCTCTCTCCACTGAC 847
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QY 848 ATTCCTGCTCTTACAGAAAGGAACTATGAACTTTTACAGACCAAGAAATTAAGCA 907
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QY 1148 ACAACCG 1154
DB 1148 AACACAG 1154

RESULT 5
LOCUS AX139113 1173 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 1 from Patent EP1096009.
ACCESSION AX139113
VERSION AX139113.1 GI:14274791
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 Peter, B. and O'Reilly, M. A.
AUTHORS G-protein coupled receptor-1 like polypeptide
TITLE Patent: EP 1096009-A 1 02-MAY-2001;
JOURNAL Pfizer Limited (GB) ; PFIZER INC. (US)
FEATURES
source location/Qualifiers
1..1173
/organism="Homo sapiens"
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ORIGIN

Query Match 57.7%; Score 675; DB 6; Length 1173;
Best Local Similarity 74.9%; Pred. No. 2.7e-159;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAATTAACAGTACATCCGCTTAACATCAATTAATTTCTTGAATTTTAATGCTT 67
DB 11 CTAATAGCAATTCATTTATCATCAGACATCGTGTAATTTAGCATTTTATGTCCT 70
QY 68 TACTAGCTATTGCTTAATAGTTAGGCAATGCTGTCATTTTATTTATTTAGTACA 127

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Db 131 AAAACCTTAGACATGCAAGTAATTTTCTTAACCTTGGCATTGCAAGCTTCTTG 190
Qy 188 TGGGTGCAATTTGCAATTTCTGTAGACCTTCCGTGGGACTTCTGTGACTTGTGAA 247
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Qy 308 ATATTGCTCATCAGCTAGATGCTGACAGTCTTCAAAATGCCGTGTGTATAGAG 367
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Qy 368 CTCAGACCTGCGACCTGGAAAATGCTAGATGGGTGGTGTGTGTATTCCTCT 427
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Db 668 TCTGTGAGACCTCATTCAGAGTAGACTTATCTTCAAGAGATCTTTCTGACATCAGAG 727
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Qy 1148 ACAACCG 1154

Db 1148 AACACAG 1154
RESULT 6
AX301763 1173 bp DNA linear PAT 30-NOV-2001
LOCUS Sequence 1 from Patent WO0185786.
DEFINITION AX301763
ACCESSION AX301763
VERSION AX301763.1 GI:117382844
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jones, P. G., Blatcher, M., Wu, S. and Pausch, M. H.
TITLE Human histamine h 4? receptor
JOURNAL Patent: WO 0185786-A 1 15-NOV-2001;
American Home Products Corporation (US)
FEATURES
source location/Qualifiers
1..1173
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
Query Match 57.7%; Score 675; DB 6; Length 1173;
Best Local Similarity 74.9%; Pred. No. 2, 7e-159;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;
Qy 8 CAATACAGTACCAATCGCCTTAACATCAATTAATTTCTTGAATTTTATGCTT 67
Db 11 CTATAGCAATCAATTTATCTACTAGACATGCTGTACTTTAGATTTTATGTCTT 70
Qy 68 TACTAGCTATTTGCTATTAATTTAGGCAATGTGCGTCAATTTTATTTATTTGGACA 127
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Qy		908	AGTCACTGCGCCATACTCTTAGCAGCT	TTTGGCATTTGCTGGGCTTCATATTCACGTACTA	967
Db		908	AGTCACTGCGCATTCCTTTAGGGGTT	TGTGGCTTTGGCTGGGCTTCATATTCGTGTTCA	967
Qy		968	CAGTTATCTACTCATTTTCTCTGAAAG	AACTGACTTAATTCAACTGTAACCACTACTG	1027
Db		968	CAAATGTCTCTTCATTTATTTCTCAG	CAAGCGTCTTAAATCAATTTGGTATGAAATGG	1027
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Qy		1148	ACAACCG	1154	
Db		1148	AACACAG	1154	
RESULT 7					
LOCUS		BD015847	1173 bp	DNA	linear
DEFINITION		Novel polypeptide.			PAT 27-AUG-2002
ACCESSION		BD015847			
VERSION		BD015847.1			GI:22556984
KEYWORDS		JP 2001211889 -A/1.			
SOURCE		Homo sapiens (human)			
ORGANISM		Homo sapiens			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
TITLE		1 (bases 1 to 1173)			
JOURNAL		Peter B. and Olaylee,M.A.			
COMMENT		Novel polypeptide			
		Patent: JP 2001211889-A 1 07-AUG-2001;			
		PFIZER INC			
		OS Homo sapiens (human)			
		PN JP 2001211889 -A/1			
		PD 07-AUG-2001			
		PF 27-OCT-2000 JP 2000329359			
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		BEST PETER,BK ANTONY OLAYLEE			
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		PC C07K14/00,			
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Best Local Similarity	74.9%; Pred. No. 2.7e-159;	
Matches 859; Conservative	0; Mismatches 285; Indels 3; Gaps 1	
Qy	8 CAAATTAACAGTACATCGCCTTAAACATCAATTAATAAATTTCTTGACATTTTAATGCTT	67
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Qy	68 TACTAGCTATTGCTATAATGTTTAGGCAATGTCGTGCTCATTTTAGCTTTATTGTGACA	127
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Qy	428 TCATGACAAATGGGCGCATGATTCGATTTGACACTCTTTGGCAGATAAGCACTACAGAA	487
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Qy	608 GAGAGAACTGAGCAGGTGCTCTCAGCCCAACCTGTACTCCCTCTGATCTTCCAGCAGTG	667
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Qy	668 AACACGCACTCTCTGAGCAGACAGACCCCGATTTCAAGGCCCATCTGCCACAGACGAAAG	727
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Qy 1148 ACAACCG 1154
Db 1148 AACACAG 1154

RESULT 8

AF307973 1173 bp mRNA linear PRI 14-NOV-2000
LOCUS Homo sapiens histamine H4 receptor mRNA, complete cds.

DEFINITION AF307973
ACCESSION AF307973
VERSION AF307973.1 GI:1141732
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1173)
AUTHORS Jones, P.G., Wu, S. and Betty, M.
TITLE Cloning of a novel histamine receptor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1173)
AUTHORS Jones, P.G., Wu, S. and Betty, M.
TITLE Direct Substitution
JOURNAL Submitted (25-SEP-2000) Neuroscience, Wyeth Ayerst, CN8000, Princeton, NJ 08543, USA

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ORIGIN

Query Match 57.7%; Score 675; DB 9; Length 1173;
Best Local Similarity 74.9%; Pred. No. 2.7e-159; Indels 3; Gaps 1;
Matches 859; Conservative 0; Mismatches 285;

Qy 8 CAAATAACAGTACATCGCCTTAACATTAATAATTTCTTGACATTTTATGCTT 67
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Qy 308 ATATGCTCATACAGCATCTGCTACAGTCTGCTCAATATGCGTGTGTATAGAG 367
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Qy 368 CTCAGCATCTGACCTGGAAATTTGCTACATGCTGTGCTGTGTGATATCTCT 427
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Qy 428 TCATGCAAAATGGGCGGATGATCTGATTCAGACTCTGGGCGAATPAGCATACGAAT 487
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Qy 668 ACCACGAGACTCTCTGACAGAGAGCCCGATTCAGAGGCACTGCGCAGCAGGAAG 727
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Qy 728 AAACAACTGCTCTCTTGGTTGACAGAGTACGAGAGAAAGAGAGCTCTTGTTCGA 787
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Db 1148 AACACAG 1154

RESULT 9
AF325356 1173 bp mRNA linear PRI 11-SEP-2001
LOCUS Homo sapiens histamine receptor H4 (XOR35) mRNA, complete cds.
DEFINITION AF325356
ACCESSION AF325356.1 GI:155532602
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1173)
Zhu, Y., Michalovich, D., Wu, H.-L., Tan, K. B., Dycko, G. M.,
Mannan, I. D., Boyce, R., Alston, J., Tierney, L. A., Li, X.,
Herzily, N. C., Vawter, L., Sarau, H. M., Ames, R. S., Davenport, C. M.,
Hieble, P., Wilson, S., Bergsma, D. J. and Fitzgerald, L. R.
Cloning, expression, and pharmacological characterization of a
novel human histamine receptor
Mol. Pharmacol. 59 (3), 434-441 (2001)
JOURNAL
MEDLINE 21106320
PUBMED 11179436
REFERENCE 2 (bases 1 to 1173)
Zhu, Y., Michalovich, D. and Fitzgerald, L. R.
Direct Submission
Submitted (30-NOV-2000) Genbank, 709 Swedeland Rd., PO Box
1539, King of Prussia, PA 19406, USA
JOURNAL
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ORIGIN
Query Match 57.7%; Score 675; DB 9; Length 1173;
Best Local Similarity 74.9%; Pred. No. 2.7e-159;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;
QY 8 CAAATACAGTACATCGCCTTAACATCAATTAATTTCTTGACATTTTAAATGCTT 67
DB 11 CTAATAGCAATCAATTTATCACTAAGCATCGGTACTTAGCATTTTATGCTCT 70
QY 68 TACTAGCTATGCTAATAGTATAGGCAATGCTGGTCACTTTAGCTTTATTTGGACA 127
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DB 1148 AACACAG 1154

RESULT 10
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LOCUS Homo sapiens histamine receptor H4 mRNA, complete cds.
DEFINITION AF329449
ACCESSION AF329449.1 GI:13876643
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1173)
 AUTHORS Morse, K.L., Behan, J., Laz, T.M., West, R.E. Jr., Greenfeder, S.A.,
 Anthes, J.C., Unland, S., Yan, Y., Hipkin, R.W., Gonsiorek, W., Shin, N.,
 Gustafson, E.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M.,
 and Monema, F.J. Jr.
 TITLE Cloning and characterization of a novel human histamine receptor
 J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)
 JOURNAL MEDLINE
 PUBMED 21104636
 REFERENCE 2 (bases 1 to 1173)
 AUTHORS Monema, F.J. Jr., Wang, S., Behan, J., Laz, T.M., Greene, J. and
 Bayne, M.
 TITLE Direct Submission
 JOURNAL Submitted (15-DEC-2000) Human Genomics Research, Schering-Plough
 Research Institute, 2015 Galloping Hill Rd., Kenilworth, NJ 07033,
 USA

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ORIGIN
 Query Match 57.7%; Score 675; DB 9; Length 1173;
 Best Local Similarity 74.9%; Pred. No. 2.7e-159; Indels 3; Gaps 1;
 Matches 889; Conservative 0; Mismatches 285;

QY 8 CAAATACAGTACATCGCCTTAACATCAATTAATTTCTTGACATTTTATGTCCT 67
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 QY 68 TACTAGTATGCTATATATTTAGGCAATGTCGTGCTATTTAGCTTTATTTGTGACA 127
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 QY 548 TGAATCCCATCTTGTAGTTGCTTATTTCAAGGCCCATATTTACTGAGGCTTGGAAAGC 607
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RESULT 11
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 DEFINITION Homo sapiens histamine receptor H4 (H4) mRNA, complete cds.
 ACCESSION AY008280
 VERSION AY008280.1 GI:15822540
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1173)
 Nguyen, T., Shapiro, D. A., George, S. R., Setola, V., Lee, D. K.,
 Cheng, R., Rauser, L., Lee, S. P., Lynch, K. R., Roth, B. L. and
 O'Dowd, B. F.
 TITLE Discovery of a novel member of the histamine receptor family
 JOURNAL M.O.L. Pharmacol. 59 (3), 427-433 (2001)
 MEDLINE 21106319
 PUBMED 11179435
 REFERENCE 2 (bases 1 to 1173)
 Nguyen, T., George, S. R., Lee, D. K., Cheng, R., Lynch, K. R. and
 O'Dowd, B. F.
 TITLE Discovery of H4, a Novel Histamine Receptor
 JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1173)
 AUTHORS Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and O'Dowd,B.F.
 TITLE Direct Submission
 JOURNAL Submitted (26-SEP-2000) Pharmacology, University of Toronto, 8 Taddle Creek Rd., Rm. 4353, Toronto, Ont M5S 1A8, Canada
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ORIGIN

Query Match 57.7%; Score 675; DB 9; Length 1173;
 Best Local Similarity 74.9%; Pred. No. 2.7e-159;
 Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATPACAGTCAATCGCCTTAACATCAATTAATTTCTTGACATTTTAATGCTT 67
 DB 11 CTAATAGCAATCAATTTATCACTAGACACTCGGTGTAATTGATTTTATGTCCT 70
 QY 68 TACTAGCTATTGCTAATAGTATAGCAATGTCGTGCTATTGAGCTTTATTTGAGCA 127
 DB 71 TAGTAGCTTTTGTCTAATAGTAGCAAAAGCTTTGCTCATTTTAGCTTTTGTGTGGACA 130
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 QY 788 TAAAGCTTACAAAGAACAGCAATGATGCTGCTTCCAAATGGCTTCTTCCACTCAG 847
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 QY 848 ATTCCCTGCTCTTCAAGAAAGGAAACATTCGAATCTTTACAGCCACGAAATTAAGCA 907
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 QY 1088 AACGTTTCAGAAAGCTTTCCTGAAATATACCTTCGTGGAAGAGCAATCCAGCCACG 1147
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 DB 1148 AACACAG 1154

RESULT 12
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 LOCUS AY136745
 DEFINITION Homo sapiens histamine receptor H4 (HRH4) mRNA, complete cds.
 ACCESSION AY136745
 VERSION AY136745.1 GI:22658472
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1173)
 AUTHORS Puhl,H.L. III, Ikeda,S.R. and Aronstam,R.S.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUL-2002) cDNA Resource Center, Guthrie Research Institute, One Guthrie Square, Sayre, PA 18840, USA
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ORIGIN

Query Match 57.7%; Score 675; DB 9; Length 1173;
Best Local Similarity 74.9%; Pred. No. 2,7e-159;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAATAACAGTACATCGCTTAACATCAATTAATTTCTTGACATTTTATGCTT 67
DB 11 CTATATGCAACATCAATTTATCACTAAGCACTGCTGTTACTTTAGCATTTTATGCTT 70
QY 68 TACTAGCTATGCTATATATGTTAGGCAATGCTGCTGATTTTATGTTAGTACA 127
DB 71 TAGTACCTTTGCTATATATGCTAGGAATGCTTTGGTCATTTTATGTTAGTACA 130
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QY 188 TGGGTCAATTTGCAATTTCTCTGTAACATACCTTCTGCTGACTTACTGACTTTGAA 247
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DB 371 CTCACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 430
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DB 1088 AGGCTTCAAG 1147
QY 1148 ACAACCG 1154
DB 1148 AACACAG 1154

RESULT 13
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LOCUS
DEFINITION Homo sapiens mRNA for histamine receptor H4 (HRH4 gene).
ACCESSION AJ298292
VERSION AJ298292.1 GI:18152452
KEYWORDS histamine receptor H4; HRH4 gene.
SOURCE
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS O'Reilly, M.A.
TITLE Identification of a histamine H4 receptor on human eosinophils -
unpublished
JOURNAL 2 (bases 1 to 1173)
AUTHORS O'Reilly, M.A.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2001) O'Reilly M.A., Discovery Biology, Pfizer
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ORIGIN

Query Match 57.7%; Score 675; DB 9; Length 1173;
Best Local Similarity 74.9%; Pred. No. 2,7e-159;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAATAACAGTACATCGCTTAACATCAATTAATTTCTTGACATTTTATGCTT 67

11 CTAATAGACATTCATTTATCTAAGACACTGCTTACTTATGACATTTTATGCTCT 70
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AX376577
LOCUS
DEFINITION Sequence 5 from Patent WO0200719.
ACCESSION AX376577
VERSION AX376577.1 GI:19170678
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Lin,D.C., Zhao,J., Chen,J.L. and Cutler,G.
AUTHORS Novel receptors
TITLE Patent: WO 0200719-A 5 03-JAN-2002;
JOURNAL Tularik Inc. (US)
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Query Match 57.7%; Score 675; DB 6; Length 1266;
Best Local Similarity 74.9%; Pred. No. 2.7e-159;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;
Qy 8 CAAATTAACAGTACATTCGCTTAACTAATTAATTTCTTGAATTTTAAATGCTT 67
Db 35 CTAATAGACATTCATTTATCTAAGACACTGCTTACTTATGCTTTTATGCTCT 94
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Db 95 TAGTAGCTTTTCTTAATAGTGAAGATGCTGCTATTTTACTTTTGGGAGACA 154
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428 TCATGACAAATGGGCGGATGATTCGATTCAGACTCTTGGCAGAAATAGCACTACGAAT 487
455 TCTTAGTGAATGGCCAAATATTTCTAGTTCTAGAGTCTTGGAAAGATGAGTGAAT 514
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692 TCTGTGAGACACTATTCAGAGGTAGATCTATCTTCAAGAGATCTCTTCTGATCGACAG 751
728 AAACAACTGCTCTCTTGTTCAGACAACTGACGAGAGAAAGACAGTCTCTTGTTCGA 787
752 AAGTTCCTGATCTCTTCTTATTCAGAGAGACAGAGAGAAAGATGATCTCATGTTTTCT 811
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812 CAAGAAACCAAGATGAATGCAATGCAATGCTTCCAAATGGGCTTCCCTCCACCTCAG 871
848 ATTCCCTGCTCTTTCAGCAAGGAAACATATCGAATCTTTCAGAGCAGAGAAATTAAGCA 907
872 ATTCTGAGTCTTTCAGCAAGGAAACATGTTGAATCTTTCAGAGCAGAGATTAAGCA 931
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1148 ACAACCG 1154
1172 AACACAG 1178

RESULT 15
AX301229
LOCUS AX301229 1300 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 1 from Patent WO0185793.
ACCESSION AX301229
VERSION AX301229.1 GI:17382320
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Lind, P., Sejlitz, T., Vogel, G. and Wood, L.S.
TITLE G protein-coupled receptors
JOURNAL Patent: WO 0185793-A 1 15-NOV-2001;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES
source 1..1300

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
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Best Local Similarity 74.9%; Pred. No. 2,7e-159;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;
8 CAATATACAGTACAAATCGCTTACATCAATTAATTTCTTTGACATTTTATGCTT 67
51 CTATATGCAACAAATTAATTAATCACTAGACCTGTGTACTTTAGATTTTATGCTT 110
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111 TAGTACTTTTGTATTAATGTTAGCAATGCGGTCATTTAGCTTTATTTAGTGACA 170
128 GAAATCTTACATCAAGATTAATTAATTTTCTTAATCTTGGCAATTTGACACTTTG 187
171 AAAACCTTACATCAAGATTAATTTTCTTAATCTTGGCAATTTGACACTTTG 230
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591 TGATCCCATCTTTGTTAGTTGTTTATTCAGCCGCCATTTTACTGAGCCTGTGAAGC 650
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651 GTATGATCTGATGAGGTGCTGACGACCTGATCCCTGATCCCTTCCAGCAGTGG 707
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708 TCTGTGAGACACTATTCAGAGGTAGATCTTTCATGAGAGATCTTTCATGATCGACAG 767
728 AAACAACTGCTCTCTTGTTCAGACAACTGACGAGAGAAAGACAGTCTTGTGTTTCA 787
768 AAGTTCCTGATCTTTCATTTCAAGAGAGACAGAGAGAAAGATGATCTCATGTTTCT 827
788 TAGAGCTTACAGAAACAGCAATGTATGCTTCCAAATGGGCTTCCCTCCACCTCAG 847
828 CAAGAAACCAAGATGAATGCAATGCAATGCTTCCAAATGGGCTTCCCTCCACCTCAG 887
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908 AGTCACTGCGCAATCTTTCAGAGCTTTTGCATTTGCTGGCTCCATATTCAGTGAATA 967
948 AGTCACTGCGCAATCTTTCAGAGCTTTTGCATTTGCTGGCTCCATATTCAGTGAATA 1007

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Qy 968 CAGTATCTACTCATTTTTCCTGAAAGGAACTGACTAATCAACCTGGTACCACTACTG 1027
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Db 1008 CAATTGTCTCTTCATTTTATCTCTCAGCAACAGTCTTAATCAGTTGTATAGAAATTG 1067
    |||||
Qy 1028 CCTTTGGCTCCAGTGTCTCAATTCCTTTGTATATCCCTTTTGTATCCATTGTGTACAG 1087
    |||||
Db 1068 CATTTGGCTTCAGTGTCTCAATTCCTTTGTATATCCCTTTTGTATCCATTGTGTACAG 1127
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Qy 1088 AACGTTTCAGAAAGGCTTCTGAAAAATACTTCTGTGAGAAAGCAATCCACGCCACACAG 1147
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Qy 1148 ACAACCG 1154
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Db 1188 AACACAG 1194
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Search completed: August 5, 2005, 19:13:36
 Job time : 5073 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 15:08:34 ; Search time 653 Seconds
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Title: US-10-626-398-7

Perfect score: 1170

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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9: geneseqn2003bs:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	675	57.7	1170	3	AAAD55126	Aad55126 Human H4
3	675	57.7	1173	3	AAAD46023	Aad46023 Human G P
4	675	57.7	1173	3	AAAD01124	Aad01124 Human GPC
5	675	57.7	1173	4	AAAF83203	Aaf83203 Human GPC
6	675	57.7	1173	5	AAH24007	Aah24007 Human G P
7	675	57.7	1173	6	ABZ80663	Abz80663 Human his
8	675	57.7	1173	6	ABO78739	Abq78739 Nucleotide
9	675	57.7	1173	6	AAI70980	Aai70980 Human his
10	675	57.7	1173	6	AAI67750	Aai67750 Human his
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13	675	57.7	1173	10	ABSS57063	Abss57063 Human GPC
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16	675	57.7	1173	12	ADH88375	Adh88375 Novel hum
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20	675	57.7	1300	6	ABA02496	Abao2496 Human G p

21	675	57.7	1312	4	AAH47911	Aah47911 Human G P
22	675	57.7	3689	8	ABZ42573	Abz42573 Human his
23	675	57.7	3689	12	AD005719	Ado05719 Human his
24	675	57.7	3689	12	AD029967	Ado29967 Human GPC
25	671.8	57.4	1227	4	AAI66009	Aai66009 Human GPC
26	671.8	57.4	1265	6	AAAS98078	Aas98078 Human DNA
27	671.8	57.4	1265	6	AAAD55125	Aad55125 Human H4
28	616.8	52.7	1176	6	AAI70982	Aai70982 Rat histe
29	613	52.4	1176	6	AAI70981	Aai70981 Mouse his
30	613	52.4	1538	12	AD030257	Ado30257 Mouse GPC
31	508.6	43.5	1166	9	AAAD55124	Aad55124 Human H4
32	438.8	37.5	1103	3	AAAD55123	Aad55123 Human H4
33	270.8	23.1	540	6	AAAS98150	Aas98150 Human G-P
34	270	23.1	1326	6	AAAD3667	Aad3667 Human G-P
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36	138	11.8	721	5	AAAS43459	Aas43459 Human G-P
37	132.2	11.3	1239	2	AAAX84570	Aax84570 G-protein
38	132.2	11.3	1239	3	AAAX84571	Aax84571 G-protein
39	132.2	11.3	2700	3	AAAX84571	Aax84571 G-protein
40	132.2	11.3	2700	3	AAAX84571	Aax84571 G-protein
41	124.2	10.6	1311	9	AAAS9979	Aas9979 Human H3
42	123	10.5	1338	2	AAH44575	Aah44575 Rat musca
43	123	10.5	1338	12	ADP66834	Adp66834 Murine hi
44	123	10.5	1953	3	AAAT0638	Aat0638 Rat G-pro
45	123	10.5	2761	10	ABT42301	Abt42301 Toxicity

ALIGNMENTS

RESULT 1	AAI70983	standard; cDNA, 1170 BP.
ID	AAI70983	
XX	AAI70983	
AC	AAI70983	
XX	18-MAR-2002 (first entry)	
DT	18-MAR-2002 (first entry)	
XX	Guinea pig histamine H4 receptor cDNA.	
DE	Guinea pig histamine H4 receptor cDNA.	
KW	Histamine H4 receptor; guinea pig; antiaesthetic; anti-allergenic;	
KM	anti-inflammatory; cardiac; circulatory; antidiabetic; laxative;	
KM	diagnosis; gene therapy; ss.	
XX		
OS	Cavia porcellus.	
XX		
PN	W0200192485-A1.	
XX		
PD	06-DEC-2001.	
XX		
PF	22-FEB-2001; 2001MO-US005914.	
XX		
PR	31-MAY-2000; 2000US-0208260P.	
PA	(ORTH) ORTHO-MCNEIL PHARM INC.	
XX		
PI	Lovenberg T, Liu C;	
XX		
XX	WPI; 2002-114339/15.	
DR	P-PDSB; AAM50567.	
XX		
PT	New mammalian histamine H4 receptor proteins and polynucleotides encoding	
PT	the proteins, useful in gene therapy for treating diseases where it is	
PT	beneficial to elevate mammalian histamine H4 receptor activity.	
XX		
PS	Claim 4; Fig 6B; 92pp; English.	
XX		
CC	The present sequence is that of a cDNA clone encoding guinea pig	
CC	histamine receptor of the H4 subtype. The cDNA was isolated from a bone	
CC	marrow cDNA library. It shows 75.6% homology to the human H4 receptor	
CC	coding region. The invention provides mammalian (human, mouse, rat and	
CC	guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-	
CC	83) and polypeptides (see AAM50564-67). The nucleic acids have been	

expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the mammalian histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity

Sequence 1170 BP; 301 A; 286 C; 221 G; 362 T; 0 U; 0 Other;

Query Match 100.0%; Score 1170; DB 6; Length 1170;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 TTCTTTGGGGTGCAATTTGCAATTCCTCTGTACATACCTTCTCGCTGACTTAC 240
DB 181 TTCTTTGGGGTGCAATTTGCAATTCCTCTGTACATACCTTCTCGCTGACTTAC 240
QY 181 TTCTTTGGGGTGCAATTTGCAATTCCTCTGTACATACCTTCTCGCTGACTTAC 240
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DB 601 TGAAGCGAGAAATCTGAGAGAGTGCCTCAGCCACCTGTACTCCCTGTACTCTTCC 660
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DB 1081 TGTCAAAAGCTTTTCAAGAGGCTTCTGAAAAAATCTTCTGTGAGAAAGCAATCCAG 1140
QY 1141 CCACCACAAACCGCTCAATATCCACTTGA 1170
DB 1141 CCACCACAAACCGCTCAATATCCACTTGA 1170

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RESULT 2
AADS5126
ID AADS5126 standard; DNA; 1170 BP.

AADS5126;

07-AUG-2003 (first entry)

Human H4 receptor w1d-type DNA #2.

Human; H4; histamine receptor; inflammatory bowel disease; psoriasis;
atopic dermatitis; stroke; myocardial infarction; migraine; allergy;
chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;
rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;
asthma; receptor; gene; ds.

OS Homo sapiens.

Key Location/Qualifiers

FT 1..1170

FT CDS /product= "Human H4 protein"

FT /note= "CDS does not include stop codon"

FT /partial

WO2003020907-A2.

13-MAR-2003.

30-AUG-2002; 2002WO-US027891.

31-AUG-2001; 2001US-0316762P.

13-NOV-2001; 2001US-0332697F.

(MERI) MERCK & CO INC.

Gallagher MJ, Yates SL;

WPI; 2003-290186/28.

P-PsDB; AAB36417.

Novel splice variants of human H4 histamine receptor, H4b and H4c, useful

for identifying agonists or antagonists of the receptor which are useful

for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.

Disclosure; Page 56-58; 31pp; English.

The invention relates to splice variants of human H4 histamine receptor.

CC H4b and H4c. The invention is useful for identifying an agonist, antagonist or inverse agonist of a mammalian histamine receptor. The CC agonist, antagonist or inverse agonist of H4b and H4c is useful for treating inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease, or psoriasis. The present sequence is human H4 receptor DNA

Sequence 1170 BP; 292 A; 245 C; 231 G; 402 T; 0 U; 0 Other;

Query Match 57.7%; Score 675; DB 9; Length 1170;
Best Local Similarity 74.9%; Pred. No. 3,5e-190;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

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QY 8 CAATATACGATACGACCTTAACTAATTAATTTCTTGACATTTTAAATGCTT 67
DB 11 CTATATGCAATCAATTTATCACTAGACACTGCTGTTACTTATGACATTTTATGCTT 70
QY 68 TACTAGCTATGCTATATATGTTAGGCAATGCTGGTCATTTTATGTTAGGACA 127
DB 71 TATGACTTTTGTCTATATATGCTAGAAATGCTTGGCATTTTATGCTTGTGACCA 130
QY 128 GAAATTTAGACATCGAATTAATTTCTTTTCTTAACTTGGCCATTGACACTTCTTG 187
DB 131 AAAACCTTAGACATCGAATTAATTTCTTTTCTTAACTTGGCCATTGACACTTCTTG 190
QY 188 TGGTGCAATGGAATTCCTCTGTACATACCTTCCCTGCTGACTTACTGACTTCTTGGA 247
DB 191 TGGTGCAATGGAATTCCTCTGTACATACCTTCCCTGCTGACTTACTGACTTCTTGGA 250
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DB 491 GTGAACTGGAATTTTAAAAAGTGTACTTGTCTCTCCCTACATCATTTATGAAATGCC 550
QY 548 TGAATCCCATCTTGTATGCTTATTTGCTTATTTGAGCGCCATATTTACTGAGGCTGTGAA 607
DB 551 TGAATCCCATCTTGTATGCTTATTTGCTTATTTGAGCGCCATATTTACTGAGGCTGTGAA 610
QY 608 GAGAGAAATGAGCAGGCTGCTGAGCACCCTGTAATCCCTGTAATCTTCCAGCAGTGG 667
DB 611 GTGATATCTCAATAGTGTGCAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 667
QY 668 ACCAGCAGACCTCTGCTGAGCAGGACCCGATTTCAAGGGGACTGTGCGACAGCGAAAG 727
DB 668 TCTGTGAGACCTATTCAGAGTAGATATCTTCAAGAGATATCTTTTGTGATGACAG 727
QY 728 AAACAACTGCTCTCTTGTGTGACAGCAATGCAAGGAAAGACAGTCTTGTGTTTCCA 787
DB 728 AAGTTCCTGATCTTTTCAATTCAGAGAGACAGAGGAAAGATAGTCTATGTTTCTT 787
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QY 908 AGTCACTGGCCATACCTTTAGCAGCTTTTGCATTTGCTGGCTCCATATTCAGTACTA 967
DB 908 AGTCACTGGCCATACCTTTAGCAGCTTTTGCATTTGCTGGCTCCATATTCAGTACTA 967
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DB 1088 AGCGCTTTCGAAAGGCTTCTTGAATAATTTTGTATTAAGCAACCTCTACATCAC 1147
QY 1148 ACAACCG 1154
DB 1148 AACACAG 1154

RESULT 3
AAA46023
ID AAA46023 standard; cDNA; 1173 BP.
XX
AC AAA46023:
XX
DT 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13.
XX
KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;
KW se.
XX
OS Homo sapiens.
XX
PN WO200022131-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WC-US024065.
XX
PR 13-OCT-1999; 98US-00170496.
PR 12-NOV-1998; 98US-0108029P.
PR 20-NOV-1998; 98US-0109213P.
PR 27-NOV-1998; 98US-0110060P.
PR 16-FEB-1999; 98US-0120416P.
PR 26-FEB-1999; 98US-0121852P.
PR 12-MAR-1999; 98US-0123944P.
PR 12-MAR-1999; 98US-0123945P.
PR 12-MAR-1999; 98US-0123946P.
PR 12-MAR-1999; 98US-0123948P.
PR 12-MAR-1999; 98US-0123949P.
PR 12-MAR-1999; 98US-0123951P.
PR 28-MAY-1999; 98US-0136436P.
PR 28-MAY-1999; 98US-0136437P.
PR 28-MAY-1999; 98US-0136439P.
PR 28-MAY-1999; 98US-0137127P.
PR 28-MAY-1999; 98US-0137131P.
PR 28-MAY-1999; 98US-0137567P.
PR 28-JUN-1999; 98US-0141448P.
PR 27-AUG-1999; 98US-0151114P.
PR 03-SEP-1999; 98US-0152524P.
PR 29-SEP-1999; 98US-0156555P.
PR 29-SEP-1999; 98US-0156633P.
PR 29-SEP-1999; 98US-0156634P.
PR 29-SEP-1999; 98US-0156653P.
PR 01-OCT-1999; 98US-0157280P.
PR 01-OCT-1999; 98US-0157281P.
PR 01-OCT-1999; 98US-0157282P.
PR 01-OCT-1999; 98US-0157293P.

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PR 01-OCT-1999; 99US-0157294P.
 PR 12-OCT-1999; 99US-00416760.
 PR 12-OCT-1999; 99US-00417044.
 XX
 PA (AREN-) ARENA PHARM INC.
 PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT,
 PI Gore M, Iliaw CW, Lin I, Lowitz K, White C;
 DR WPI: 2000-117986/27.
 DR P-PSDB; AAB02831.
 XX
 PT Non-endogenous, human G protein-coupled receptors for screening receptor,
 PT Inverse or partial agonists useful as therapeutic agents.
 XX
 PS Example 1; Page 88-89; 187p; English.
 XX
 CC The present invention describes transmembrane receptors, preferably human
 CC G protein coupled receptors (GPCR), for which the endogenous ligand is
 CC unknown (orphan GPCR receptors). More specifically the present invention
 CC relates to non-endogenous, constitutively activated versions of a human
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct
 CC identification of candidate compounds as receptor agonists, inverse
 CC agonists or partial agonists for use as pharmaceutical agents. AAB46017
 CC to AAB46126 and AAB02825 to AAB02859 represent sequences used in the
 CC exemplification of the present invention
 CC
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
 Query Match 57.7%; Score 675; DB 3; Length 1173;
 Best Local Similarity 74.9%; Pred. No. 3.5e-190;
 Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 608 GAGAGAACTGAGAGAGTGGCTCAGCCACCCTGTACTCCCTCTGACTCTTCCAGAGT 667
 DB 611 GTGATCATCTCAGTAGGAGGCGCAAGGCATCTCGACTGACTGCTCTTCCAAACA --- 667
 QY 668 ACCACGACATCTCTGCGACAGACAGACCCCGATTCAAGGCGCACTTGGCAGACGGAAG 727
 DB 668 TCTGAGACACTCATTCAGAGTAGACTATCTTCAAGAGATCTCTTCTGATCGACAG 727
 QY 728 AAACACTGCGCTCTTGGTTCAGACAGTCAAGGAGAAAGACAGTCTCTGTTTCCCA 787
 DB 728 AAGTTCTGCACTCTTTCATTCAAGAGACAGAGAGAAAGATGCTCATGTTTCT 787
 QY 788 TAAGAGCTCAAGAAACGACAAATGATCGCTTCCAAATGAGGCTTCTTCCCATG 847
 DB 788 CAAGAACCAAGATGAATGACAAATGCTTCCAAATGAGGCTTCTTCCCATG 847
 QY 848 ATTCCCTGCTTCAGAAAGGAAACATTCGAACTTTTCAAGCCAGAAATTAGCA 907
 DB 848 ATTCTGATGCTTTCACAAAGGGAACATTTGAATCTGTAGAGCCAGAGATTAGCA 907
 QY 908 AGTCAGTGGCATACTCTTACAGCTTTCGCAATTTGCTGGGCTTCATATTCAGTACTA 967
 DB 908 AGTCACTGGCATTCCTTAGGGGTTTGTCTGTTGCTGGGCTTCATATTCCTGTTCA 967
 QY 968 CAGTTATCTACTATTTTCTCTGAAGAACTGACTTAAATCAACTGTGTAACACTG 1027
 DB 968 CAATTGCTCTTCAATTTATTCCTCAGCAAGGCTTAAATCAAGTTGTAATGAAATTG 1027
 QY 1028 CCTTTGGCTCAGAGGTCAATTCCTGTAATCCCTTTTGTATCATTTGATGTCACA 1087
 DB 1028 CATTTGGCTCAGAGGTCAATTCCTGTAATCCCTTTTGTATCATTTGATGTCACA 1087
 QY 1088 AACGTTTTCAGAAAGCTTTCCTGAAATATCTCTGTGAGAAAGGACCAAGCCAGC 1147
 DB 1088 AGCGCTTCAAAAGGCTTCTTGAATAATTTTGTATATAAAGAACCTTACATCAC 1147
 QY 1148 ACAACCG 1154
 DB 1148 AACACAG 1154

RESULT 4
 AAD01124
 ID AAD01124 standard; cDNA; 1173 BP.
 XX
 AC AAD01124;
 XX
 DT 02-NOV-2000 (first entry)
 XX
 DE Human orphan G protein-coupled receptor hrup7 cDNA.
 XX
 KW Human; orphan G protein-coupled receptor; GPCR; hrup7; drug screening;
 KW transmembrane receptor; signal cascade; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1173
 FT /tag= "a"
 FT /product= "hrup7"
 FT /note= "Human orphan G protein-coupled receptor"
 PD WO200031258-A2.
 PD 02-JUN-2000.
 PF 13-OCT-1999; 99WO-US023687.
 XX
 PR 20-NOV-1998; 98US-0109213P.
 PR 16-FEB-1999; 99US-0120416P.
 PR 26-FEB-1999; 99US-0121852P.
 PR 12-MAR-1999; 99US-0123946P.
 PR 12-MAR-1999; 99US-0123949P.

DT	10-AUG-2001 (first entry)
XX	
XX	Human G protein-coupled receptor AXOR35 cDNA.
KM	AXOR35; human, G protein-coupled receptor; 7TM receptor;
KW	histamine H3 receptor homologue; infection; viral; bacterial; fungal;
KM	protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
KM	bulimia; osteoporosis; asthma; allergy; urinary retention;
KM	acute heart failure; hypotension; hypertension; angina pectoris;
KM	myocardial infarction; stroke; ulcer; migraine; vomiting;
KM	psychotic disorder; neurological disorder; anxiety; schizophrenia;
KM	manic depression; bipolar disorder; depression; delirium; dementia;
KM	severe mental retardation; dyskinesia; Parkinson's disease;
KM	Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;
KM	macrophage; eosinophil; neutrophil; function modulation;
KM	autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
KM	drug screening; signal transduction; transgenic animal; drug discovery;
KM	ss.
OS	
XX	Homo sapiens.
XX	
FH	Location/Qualifiers
FT	1..1173
FT	/*tag=a
FT	/product= "Human AXOR35"
FT	/note= "G protein-coupled receptor"
XX	
PN	M0200133221-A1.
PD	
XX	10-MAY-2001.
XX	
PF	26-OCT-2000; 2000MO-US029461.
XX	
PR	02-NOV-1999; 99US-00431898.
PR	03-FEB-2000; 2000US-00497790.
XX	
PA	(SMIK) SMITHKLINE BEECHAM CORP.
PA	(SMIK) SMITHKLINE BEECHAM PLC.
PI	Aubart KM, Bergema DJ, Fitzgeraid LR, Graybill TL, Li X;
PI	Michalovich D, Morrow DM, Zhu Y;
DR	WPJ; 2001-316464/33.
XX	
DR	P-PSDb; AAB73622.
PT	
PT	Novel G-protein coupled receptor polypeptide and polynucleotide for
PT	treating cancer, autoimmune, pulmonary, cardiovascular and neurological
XX	disorders and for identifying modulators useful for treating asthma.
PS	
PS	Claim 2; Page 49-50; 54bp; English.
XX	
CC	The invention relates to the human G protein-coupled receptor AXOR35
CC	(AAB73621), to cDNA encoding AXOR35 (AAB4006), and to AXOR35 fragments
CC	and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative
CC	transmembrane domains and is involved in signal transduction. AXOR35 has
CC	homology and structural similarity with G protein-coupled receptors such
CC	as the human histamine H3 receptor. The invention also relates to
CC	expression vectors and host cells comprising AXOR35 DNA, to recombinant
CC	expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins
CC	and nucleotides may be used to treat a wide variety of disorders
CC	including bacterial, fungal, protozoal and viral infections, particularly
CC	HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy;
CC	diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;
CC	urinary retention; acute heart failure; hypotension; hypertension; angina
CC	pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;
CC	psychotic and neurological disorders such as anxiety, schizophrenia,
CC	manic depression, depression, delirium, dementia, and severe mental
CC	retardation, and dyskinesias, such as Parkinson's disease, Huntington's
CC	disease or Gilles de la Tourette's syndrome. AXOR35 proteins and
CC	nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and
CC	antibodies may be used in screening compounds for their ability to
CC	modulate AXOR35 activity or expression. Such AXOR35 modulators are
CC	particularly useful for treating asthma, and inhibiting or promoting the

	CC	function of lymphocytes, macrophages, eosinophils or neutrophils in
	CC	aschmatic lung.
	CC	AXOR3 proteins, nucleotides and antibodies are also
	CC	useful for diagnosing or determining susceptibility of an individual to a
	CC	disease via the detection of abnormal levels of protein or mRNA, or via
	CC	the detection of mutations in the corresponding gene.
	CC	AXOR3 proteins are
	CC	also useful for inducing an immunological response in a mammal against
	CC	the above diseases, and for antibody production.
	CC	AXOR3 nucleotides are
	CC	also useful as diagnostic reagents, in chromosome localisation and tissue
	CC	expression studies, and for producing transgenic animals useful in drug
	CC	discovery.
	CC	AXOR3-specific antibodies are useful for purifying the AXOR3
	CC	protein or fragments thereof, and are also useful for treating conditions
	CC	associated with the expression of the AXOR3 protein.
	CC	The present sequence represents cDNA encoding human AXOR3
XX		
SQ	Sequence	1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
	Query Match	57.7%; Score 675; DB 5; Length 1173;
	Best Local Similarity	74.9%; Pred. No. 3.5e-190;
	Matches	859; Conservative 0; Mismatches 285; Indels 3; Gaps 1
OY	8	CAATTAACAGTACAATGCGCTTTAAACATCAATTAAAATTCCTTGACATTTTTAATGTCTT 67
Dd	11	CTAATAGACACATCAATTAATTAATCACTAAGACACTCGGTACTTAGCATTTTTATGTCTCT 70
OY	68	TACTAGCTATTGCTATAATGTTAGGAATGTCGGGTACTATTAGCTTTTATGTGGACA 127
Dd	71	TAGTAGCTTTTGTCTATATAGCTAGAATAAGTTTGGTCATTTTAGCTTTTGTGGAGACA 130
OY	128	GAAATCTTAGACATCGAAGTAATTAATCTTTTCTTAATCTTGAGGCATTCAGACTCTTGTG 187
Dd	131	AAAACTTAGACATCGAAGTAATTAATCTTTTCTTAATCTTGAGGCATTCCTGACTCTTGTG 190
OY	188	TGGGTGCAATTCGAATTCCTCTGTACATACCCTTCCTGCTGACTTACTGACCTTCGGAA 247
Dd	191	TGGGTGATGATCCTCAATTCCTTTGTACATCCCTCACAGCTGTGGAAATGGATTTTGGAA 250
OY	248	AGCAAAGCTTGTGTATTTTGGCTCATTAAGTACTATCTTTATGTACAGACTGTGTGTATA 307
Dd	251	AGGAAATCTGTGTATTTTGGCTCATTAAGTACTATCTTTATGTACAGACTGTGTATATA 310
OY	308	AATATGTCCTCATAGCTACAGATGGCTAACAGCTCAAGTCCGCTGGTATAG 367
Dd	311	ACATTGTCCTCATAGCTACATATGATATGATACCTGTCAAGTCAATGCTGTGTATAGAA 370
OY	368	CTCAGCACTCTGGGACCTCGGAAAAATTTGGTACTCAGATGATGAGCTGTTTGGATATCTCT 427
Dd	371	CTCAACATACCTGGGGGCTTGTGAAGATGTTTACTCTGATGATGATGCGCTTTGGGCTGGCCT 430
OY	428	TCATGACAAATGGSCCGCATGATCTTGATTTCAACTCTTGGCAGATATAGCACTACAGANT 487
Dd	431	TCTTAGTGAATGGGCCAATGATCTTCAAGTTTCAAGAGTCTTGGAAAGATAGAGTATGAT 490
OY	488	GTTGAACCTGATTTTAAAAAGGTATCTTGTCTCCCAATCATTAATTTGAAATTC 547
Dd	491	GTTGAACCTGATTTTTCGGAATGTATCAATCTTGGCATCAACATCTTGTGAATTCG 550
OY	548	TGATGCCCATCTTGTAGTTCCTTATTTCAAGGCCCATATTTAATCTGAGGCTGTGGAGAGC 607
Dd	551	TGATGCCCATCTTGTAGTTCCTTATTTCAACATGATATTTATTTGAGGCTGTGGAGAGC 610
OY	608	GAGAGAACTTGAGAGGCTGCTCAAGCCAACCTGTACTCCCTCTGACTCTTCCAGCAGTG 667
Dd	611	GTTGATCATCTCAGTAGGCTGCAAGGCCATCTGTGACTGACCTGCTCTTCCAAACA--- 667
OY	668	ACCAAGCAACTCTTGAGAGAGAGAACCCCATTTCAAGGGCGCACTCTGCGACAGCGAAG 727
Dd	668	TCTGTGACATCTATCAGAGGTAGACTATCTTCAAGAGATCTCTTTCTGTGATGACAG 727
OY	728	AAACAACTGCTCTCTTGGTTCAACAAGTCAACGGAGAAAGAGAGTCTCTGTGTTTCCA 787
Dd	728	AAAGTTCTGATCTCTTTCATTCACAGAGACAGAGAGAAAGATAGTCAATGTTTCTCT 787
OY	788	TAAAGACCTTACAGAAACGACATGTGATCGCTTCAAAATGGGCTTCTCTCCACCTCAG 847

```
Db 768 CAAGAACCAAGATGATAGCATACATATGCTTCCAAAATGGGTTCTTCTCCATATG 847
Qy 848 ATTCCCTGGCTCTTCAGCAAGGAAACATATGCACTTTTCAGCCAGGAATTAGCCA 907
Db 848 ATTCTGTAGCTTTTCAACCAAGGAAACATGTTGAACTGTTAGACCCAGGAAATTAGCCA 907
Qy 908 AGTCACCTGGCCATCTTCTTAGCAGCTTTTGCATTTGCTGGGCTCCATATTCAGTACTA 967
Db 908 AGTCACCTGGCCATCTTCTTAGGAGGTTTGTGCTGTTGGGCTCCATATTCCTGTGTC 967
Qy 968 CAGTATCTACTCATTTTCTTCTGAAAGAACTTGACTTAATCAACCTGGTACCTACTG 1027
Db 968 CAGTATCTCTTTCATTTTATTTCTCGAACAAGCTCTTAACAGTTGGATAGAAATTG 1027
Qy 1028 CTTTGGCTCCAGTGGTTCATATCTTTGTTAATCCCTTTTGTATCCATTTGTGTCACA 1087
Db 1028 CATTTTGGCTCCAGTGGTTCATATCTTTGTTAATCCCTTTTGTATCCATTTGTGTCACA 1087
Qy 1088 AACGTTTTCAGAAAGCTTCTGAAATATCTTCTGTGGAAGGCAATCCAGCCACGAC 1147
Db 1088 AGCGCTTTCAAAAGGCTTCTTGAAAATATTTGTATATAAAAAAGCAACCTTACCATGAC 1147
Qy 1148 ACAACCG 1154
Db 1148 AACACAG 1154

RESULT 7
ABZ80663
ID ABZ80663 standard; cDNA; 1173 BP.
XX ABZ80663;
AC
XX
XX
DT 13-JUN-2003 (first entry)
XX
DE Human histamine receptor coding sequence.
XX
XX human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;
XX anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;
XX anti-migraine; cardiant; anti-rheumatic; anti-arthritic; antipsoriatic;
XX neuroprotective; inflammation; asthma; allergy; atopic dermatitis;
XX myocardial infarction; migraine; chronic obstructive pulmonary disease;
XX rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
XX psoriasis; receptor.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..1173
FT FT /*tag= a
FT FT /product= "Histamine receptor"
XX
XX US6204017-B1.
XX
XX 20-MAR-2001.
XX
XX 07-OCT-1999; 99US-00414010.
XX
XX 07-OCT-1999; 99US-00414010.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Behan JX, Hedrick JA, Laz TM, Monema FJ, Morse KL, Umland SP,
XX Wang S;
XX
XX WPI: 2002-442063/47.
XX
XX P-PSDB; AB098629.
XX
XX New nucleic acid encoding antigenic part of human histamine receptor,
XX useful for preparing antibodies, e.g. for treating histamine related
XX disorders.
XX
```

```
PS Example 1; Col 27-28; 19pp; English.
XX
XX This sequence represents the open reading frame for a human histamine
XX receptor (HR) designated SP914. The sequence was isolated by searching
XX databases with the sequence of known G-coupled protein receptor (GPCR).
XX The gene is used for recombinant production of HR and for preparing
XX antibodies (Ab). These Ab are used to purify HR by immunofluorescence
XX chromatography, in immunoblotting of histamine receptor, to identify cDNA
XX clones that express the receptor, as antagonist to block binding of
XX histamine (for treating any histamine-associated disorder) and to
XX generate anti-idiotypic antibodies. Agonists and antagonists of the HR
XX protein can be used in the treatment of e.g. inflammation, asthma,
XX allergy, atopic dermatitis, stroke, myocardial infarction, migraine,
XX chronic obstructive pulmonary disease, rheumatoid arthritis, multiple
XX sclerosis, inflammatory bowel disease and psoriasis
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Query Match 57.7%; Score 675; DB 6; Length 1173;
Best Local Similarity 74.9%; Pred. No. 3.5e-190;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;
Qy 8 CAATTAACAGTACATGCGCTTAACATCATTAATTTCTTGGACATTTTAATGCT 67
Db 11 CTAATGACACATCAATTATTAATCACTAGACACTCGTTTACTTACATTTTATGCT 70
Qy 68 TACTAGCTATTGCTAATAATGTTAGGCAATGTCGTGATTTTACTTTATTTAGACA 127
Db 71 TAGTAGCTTTTGTCTAATAATGCTAGGAATGCTTGTCTATTTTACTTTTGTGTGACA 130
Qy 128 GAAATCTTAGACATGAAGTAAATTTCTTTTCTTAACCTTGGCCATTGCACTTCTTG 187
Db 131 AAAACCTTAGACATGAAAGTAAATTTCTTTTCTTAACCTTGGCCATTCTGACTTCTTG 190
Qy 188 TGGGTGCAATTGCAATTCCTGTAATACCTTCCTGCTGACTTACGACTTTCGGA 247
Db 191 TGGGTGATCTCCATTCCTTGTATGATCCCTACACGCTGTGTAATGGAATTTGGA 250
Qy 248 AGCAAGCTTGTATTTTGGCTCATTTACTGACTATCTTTTATGTAACAGATCTGTAT 307
Db 251 AGGAATCTGTATTTTGGCTCATTTACTGACTATCTTTTATGTAACAGATCTGTAT 310
Qy 308 ATATTGTCTCATGACTAGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 367
Db 311 ACATGTCTCATGACTAGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 370
Qy 368 CTCAGCACTGCGGACCTGGAATAATTTGCTACTCGAGATGCTGCTGCTGCTGCTGCT 427
Db 371 CTCAGCACTGCGGACCTGGAATAATTTGCTACTCGAGATGCTGCTGCTGCTGCTGCT 430
Qy 428 TCATGACAAATGGGCGCATGATTTGATTTGAGACTCTTGGCAGAAATGACACTAGAA 487
Db 431 TCTTAGTAATGGGCGCATGATTTGATTTGAGACTCTTGGCAGAAATGAGTAGTAAT 490
Qy 488 GTGAACCTGGAATTTTAAAGTGTACTTGTCTCTCCATCATCATTTTGAATTC 547
Db 491 GTGAACCTGGAATTTTAAAGTGTACTTGTCTCTCCATCATCATTTTGAATTC 550
Qy 548 TGATCCCATCTTGTAGTGTATTTTCAAGGCGCCATTTTACATGAGGCGTGAAGC 607
Db 551 TGATCCCATCTTGTAGTGTATTTTCAAGGCGCCATTTTACATGAGGCGTGAAGC 610
Qy 608 GAGAGAACTGAGAGGCTCTGAGCCACCTGTACTCCCTCTGACTCTTCCACAGTG 667
Db 611 GAGATCATCTGAGAGGCTCTGAGCCACCTGTACTCCCTCTGACTCTTCCACAGTG 667
Qy 668 ACCACGACATCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 727
Db 668 TCTGTGACATCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 727
Qy 728 AAAACAATGCGCTCTTGTGCTGAGCAAGTCAAGGAGGAGGAGGAGGAGGAGGAGG 787
Db 728 AAGTTCTGATCTTTCATTCAGAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 787
```

QY		788	TAAAGACCTTACAAGAACGCAATGTGATCGCTTCACAAATGGGCTTCCTCCACTCAG	847
Dd		788	CAGAACCAAGATGAATAGCAATGACATTGCTTCACAAAATGGGTTCTTCTCCCATG	847
QY		848	ATTCCCTGGGCTCTTCAGCAAAGGGAACATATCGAATCTTTGCAGAGCCAGAAATTAGCCA	907
Dd		848	ATTCTGTATGCTCTTCCACCMAAGGGGAACATGTGAATGTAATGCTTAAAGCCAGAGATTAGCCA	907
QY		908	AGTACATGCGCATACTCTTAGCAGCTTTTGCCATTGTGCTGGGCTCCATATTCATGACTA	967
Dd		908	AGTACATGCGCATCTCTTAGCAGCTTTTGCCATTGTGCTGGGCTCCATATTCATGACTA	967
QY		1028	CAATTTGGCTTCAGTGGTTCAATTCCTTTGCAATTCCTTTTGTATCCATTGTGTGACA	1087
Dd		1028	CAATTTGGCTTCAGTGGTTCAATTCCTTTGCAATTCCTTTTGTATCCATTGTGTGACA	1087
QY		1088	AACGTTTTGCAGAAGGCTTCTCTGAAAAATACCTTCCTGTGAGAAAGCAATCCACGCCACAC	1144
Dd		1088	AGCGCTTTCAAAAGGCTTCTTGAAAAATATTTTGTATATAAAAAAGCAACCTCTACCATCAC	1144
QY		1148	ACAACCG 1154	
Dd		1148	AACACAG 1154	
<hr/>				
RESULT 8				
ABQ78739 standard; DNA; 1173 BP.				
XX	AC	ABQ78739;		
XX	DT	05-DEC-2002 (first entry)		
DE		Nucleotide sequence of human histamine receptor.		
KW		Human; histamine receptor; receptor; inflammation; asthma; allergy;		
KM		atopic dermatitis; stroke; myocardial infection; migraine;		
KM		chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;		
KM		multiple sclerosis; inflammatory bowel disease; psoriasis;		
KM		intracellular second messenger pathway; cellular growth rate;		
KM		hormone secretion; gene; ss.		
XX	OS	Homo sapiens.		
XX	FT	Key	Location/Qualifiers	
XX	FT	CDS	1..1173	
XX	FT		/tag= a	
XX	FT		/product= "histamine receptor"	
XX	PN	US2002098539-A1.		
XX	PD	25-JUL-2002.		
XX	Pf	19-MAR-2001; 2001US-00812216.		
XX	PR	07-OCT-1999; 99US-00414010.		
PA	(BEHA//)	BEHAN J X.		
PA	(HEDR//)	HEDRICK J A.		
PA	(LAZI//)	LAZ T M.		
PA	(MONS//)	MONSMA P J.		
PA	(MORS//)	MORSE K L.		
PA	(UMLA//)	UMLAND S P.		
PA	(WANG//)	WANG S.		
PI		Behan JX, Hedrick JA, Laz TM, Monsma PJ, Morse KL, Umland SP,		
PI		Wang S;		

DR	WPI: 2002-673827/72-
DR	P-PSDB, ABB78276.
XX	
XX	
PT	Novel mammalian histamine receptor polypeptide useful for identifying
PT	agonist or antagonist for treating diseases such as inflammation, asthma,
PT	stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.
XX	
XX	
PS	Example 1; Page 15-16; 21pp; English.
XX	
CC	The present sequence encodes a human histamine receptor. The polypeptide
CC	is useful for identifying an agonist or antagonist of a mammalian
CC	histamine receptor. It is useful as an antigen to elicit the production
CC	of antibodies. The histamine receptor polypeptide and polynucleotide are
CC	useful in the treatment and management of diseases such as inflammation,
CC	asthma, allergy, atopic dermatitis, stroke, myocardial infection,
CC	arterial, chronic obstructive pulmonary disease (COPD), Rheumatoid
CC	arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.
CC	They are also useful for modulating intracellular second messenger
CC	pathway activated through histamine receptors (cyclic-AMP, calcium,
CC	inositol phosphate and mitogen activated protein (MAP) kinases), changes
CC	in cellular growth rate, secretion of hormones, receptor-stimulated Ca ²⁺
CC	mobilization, mitogenic effects, etc
XX	
XX	
90	Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match	57.7%	Score 675	DB 6	Length 1173
Best Local Similarity	74.9%	Pred. No. 35	5E-190	
Matches	859	Conservative	0	Mismatches 285; Indels 3; Gaps 1
QY	8	CAAAATACAGTACACANTGCCCTTAAACATCAATTAATAATTTCTTTGACATTTTAAATGCTCT	67	
DB	11	CTAATAGACACATCAATTTATTCACATAGACCTCGCTGTACTTTTGTAGCATTTTAAATGATGCT	70	
QY	68	TACATAGCATTTGCTATATATGTTAGGCAATGTCGCGGCTATTTAGCTTTTATTTGAGACA	127	
DB	71	TATAGCTTTTGTCTATATATGCTAGGAATGCTTGGTCAATTTTACCTTTTGTGTGAGACA	130	
QY	128	GAATCTTTAGACATCGAAGTAATTAATCTTTTCTTTAATCTTGCCATTGSCAGACTTCTTGG	187	
DB	131	AAACCTTAGACATCGAAGTAGTATTTTCTTTAATCTTGCCACTCTGACTCTTGG	190	
QY	188	TGGGTGCATTTGCACATTCCTCTGTACACACTTCCTCGCTGACCTTACCTGACCTTCGGAA	247	
DB	191	TGGGTGTGATCTCCATTCCTTTGTACACCTTCACACGCTGTGTGCAATGGGATTTTGGAA	250	
QY	248	AGCAGAGCTTGTATTTTGGCTCATCTACTACTACTTCTTATTTGTACAGACATCTGTATTA	307	
DB	251	AGGAATCTGTATTTTGGCTCACTACTACTACTACTTCTTATTTGTACAGACATCTGTATTA	310	
QY	308	ATATTGTCCTCATCAGCTACGATGGCTACCACTGACTCTCAAATGCCGTGTGTATTAAG	367	
DB	311	ACATTGTCCTCATCAGCTATGATGATACCTGTGACTCAATGCTGTGTCTTATTAAGAA	370	
QY	368	CTCAGACCTCGGACCCCGGAATTTGCTACTCAGATGGTGGCTGTTGGATATTCCTCT	427	
DB	371	CTCAACATCTACGGGCTCTTGAAGATTTGTACTCTGATGATGATGATGATGATGATGATGAT	430	
QY	428	TCATGACAAATGGGCCGATGATTTCTGATTTGACACTCTTGSCAGATATGACCTACAGAT	487	
DB	431	TCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAAAGATGAAGGTATGTAAT	490	
QY	488	GTGAACCTGATTTTAAAAAAGGTACTTGCCTCCCTCAACATCATTAATTGGAATTC	547	
DB	491	GTGAACCTGATTTTTCGGAATGATACATCTTGCATACATCAATCTTGTGAATTCG	550	
QY	548	TGATCCCATCTTGTATGTTGCTTATTTACAGGCCCATATTTTACCTGAGGCTGTGGAAGC	607	
DB	551	TGATCCCATCTCTTGTATGTTGCTTATTTCAACATGAATATTTATTTGAGGCTGTGGAAGC	610	
QY	608	GAGGAAATCTAGCAGGTGCTCAGCCACCTGTATCTCCCTCTGTACTCTTCCAGCAGTG	667	
DB	611	GTGATCTATCTAGTAGTGCCAAAGCACCATCTGTGACGTACGTGTCTTCCAAACA---	667	

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OY 668 ACCACGACACTCTCTGACAGACAGACCCCGATTCAAGGGCGACTCTGCCAGCAGGAAG 727
DB 668 TCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTTTCGATCGACAG 727
OY 728 AAACAACCTGCTCTCTGTGTGACAGACAGTCAACGAGAAAGACATCTCTTTGTTTCCA 787
DB 728 AAGTCTCTGACATCTCTTCAATTCAGAGAGACAGAGGAGAAAGATGTCTCACTGTTTCT 787
OY 788 TAAGACCTACAAAGAACAGCAATGTGATCGCTTCCAAAATGGGCTTCCCTCCCACTCAG 847
DB 788 CAAAGAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 847
OY 848 ATTCCCTGCTCTCTGACAGAGAGAAATATGCAATCTTTCAGAGCAGAGAAATTAAGCA 907
DB 848 ATTCTGTAGCTCTTCAACCAAGAGAAATGATGATGATGATGATGATGATGATGATGATGAT 907
OY 908 AGTCACTGGCCATCTCTTACAGAGCTTTGGCCATTTGCTGGGCTCCATATTCATGACTGA 967
DB 908 AGTCACTGGCCATCTCTTACAGAGCTTTGGCCATTTGCTGGGCTCCATATTCATGACTGA 967
OY 968 CAGTATCTACTCATTTTCTCTGAAAGAGAACTGATCAATCAACCTGATCACTACTG 1027
DB 968 CAGTATCTACTCATTTTCTCTGAAAGAGAACTGATCAATCAACCTGATCACTACTG 1027
OY 1028 CCTTTTGCTCAGAGTGTCAATCTCTTGTATTCCTTTTGTATTCATGATGATGATGATGAT 1087
DB 1028 CATTGTCTCTTCAATTTTATCTCTGACAAAGCTTCAATCACTGATGATGATGATGATGAT 1087
OY 1088 AACGTTTTCAGAGAGCTTCTGAAATATCTCTGATGAGAGCAATCCAGCCACAC 1147
DB 1088 AACGCTTTCAGAGAGCTTCTGAAATATCTCTGATGAGAGCAATCCAGCCACAC 1147
OY 1148 ACAACCG 1154
DB 1148 AACACAG 1154

RESULT 9
AA170980
ID AA170980 standard; cDNA; 1173 BP.
XX
AC AA170980;
XX
DE 18-MAR-2002 (first entry)
XX
DE Human histamine H4 receptor cDNA.
XX
KW Histamine H4 receptor; human; antihistaminic; antiallergenic;
KW antiinflammatory; cardiac; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN MO200192485-A1.
XX
PD 06-DEC-2001.
XX
PF 22-FEB-2001; 2001WO-US005914.
XX
PR 31-MAY-2000; 2000US-0208260P.
XX
PA (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
PI Lovenberg T, Liu C;
XX
DR MPI: 2002-114339/15.
XX
DR P-PSDB; AAM50564.
XX
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
XX
PS Claim 4; Fig 1; 92pp; English.
```

```
XX The present sequence is that of cDNA clone pH4R encoding a human
CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone
CC marrow cDNA library. The invention provides mammalian (human, mouse, rat
CC and guinea pig) histamine H4 receptor nucleic acid molecules (see
CC AA170980-83) and polypeptides (see AAM50564-67). The nucleic acids have
CC been expressed in recombinant host cells that produce active recombinant
CC protein. The pharmacology of known histamine ligands is demonstrated.
CC Mammalian histamine H4 receptor may be used in gene therapy for the
CC treatment of diseases where it is beneficial to elevate mammalian
CC histamine H4 receptor activity. Recombinant protein is useful for
CC identifying modulators of the human histamine H4 receptor. Such
CC modulators may be useful for diagnosing, treating or preventing asthma,
CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-
CC insulin dependent diabetes mellitus, hyperglycemia, constipation,
CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Query Match 57.7%; Score 675; DB 6; Length 1173;
Best Local Similarity 74.9%; Pred. No. 3.5e-190;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;
OY 8 CAATTAACAGTAAATCCGCTTAACATCAATTAATTAATTTCTTGAACATTTTAAATGCTT 67
DB 11 CTAATAGACACATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGCTT 70
OY 68 TACTAGCTATTGCTTAATGTTAGGCAATGTCGTCATTTTAACTTTTATTTGAGACA 127
DB 71 TAGTAGCTTTGCTTAATGTTAGGCAATGTCGTCATTTTAACTTTTATTTGAGACA 130
OY 128 GAAATCTTAGACATGAATATTAATTTTCTTAATCTTGGCAATGACATCTTCTTGG 187
DB 131 AAAACCTTAGACATGAATATTAATTTTCTTAATCTTGGCAATGACATCTTCTTGG 190
OY 188 TGGGTGCAATTGCAATTTCTCTGATACATCTTCTCTGTCATTAAGTGAATCTTGGAA 247
DB 191 TGGGTGATGTCATCTCTTCTTGTATCTCTTGTACATCTCTGACACGCTGTCGATGGAATTTGGAA 250
OY 248 AGCAAGCTTGTATTTTGGCTCATTAAGTCAATCTTATTTATGACAGATCTGTGTATA 307
DB 251 AGCAATCTGATTTTGGCTCATTAAGTCAATCTTATTTATGACAGATCTGTGTATA 310
OY 308 ATATGTCCTCATGACATGACATGTCCTACAGTCAATGTCGATGATGATGATGATGATGAT 367
DB 311 ACATGTCCTCATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 370
OY 368 CTCAGACATCTGACACCTGGAATAATGTCATCAATGATGATGATGATGATGATGATGATGAT 427
DB 371 CTCAGACATCTGACACCTGGAATAATGTCATCAATGATGATGATGATGATGATGATGATGAT 430
OY 428 TCATGACAAATGGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 487
DB 431 TCTTAGTGAATGGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
OY 488 GTGAACCTGATTTTAAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 547
DB 491 GTGAACCTGATTTTAAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 550
OY 548 TGATCCCATCTTGTAGTGTATTTTCAAGGCGCATTTTACATGATGATGATGATGATGATGATGAT 607
DB 551 TGATCCCATCTTGTAGTGTATTTCAAGGCGCATTTTACATGATGATGATGATGATGATGATGAT 610
OY 608 GAGAGAACTGACAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
DB 611 GTGATCATCTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
OY 668 ACCACGACACTCTCTGACAGACAGACCCCGATTCAAGGGCGACTCTGCCAGCAGGAAG 727
DB 668 TCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTTTCGATCGACAG 727
OY 728 AAACAACCTGCTCTCTGTGTGACAGACAGTCAACGAGAAAGACATCTCTTTGTTTCCA 787
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Db 728 AGGTCCTGCATCCTTTTATTCAGAGAGACAGAGAAAGTAGTCTCATGTTTCTT 787
 Qy 788 TAGAGCCTTACAGAAACAGAAATGATGATCCCTCCAAAATGGGCTTCTCCCACTCAG 847
 Db 788 CAGAAGCCAGATGAAATAGCAATACATGCTCCAAAATGGGCTTCTCCCAATCAG 847
 Qy 848 ATTCCTGGCTCTTACAGAAAGGAAATATCGAATCTTTTACAGAGCAGAAATTTAGCCA 907
 Db 848 ATTCCTGGCTCTTACAGAAAGGAAATATCGAATCTTTTACAGAGCAGAAATTTAGCCA 907
 Qy 908 AGTCACTGGCCATCTCTTACAGAGCTTTGGCCATTTGGGCTCCATATTCATCTAGATA 967
 Db 908 AGTCACTGGCCATCTCTTACAGAGCTTTGGGCTTTGGCTCCATATTTCTGTGTCA 967
 Qy 968 CAGTTATCTACTATTTTCTTGAAGAGAACTGACTAATGACCTGTATACATACG 1027
 Db 968 CAGTTATCTCTTATTTTATTTCTTGAAGAGAACTGACTAATGAGTTGTAAGAATG 1027
 Qy 1028 CTTTGGCTCAGAGGCTTCAATTCCTTTGTATCCCTTTTGTATCCATGTGTACACA 1087
 Db 1028 CATTGGCTCAGAGGCTTCAATTCCTTTGTATCCCTTTTGTATCCATGTGTACACA 1087
 Qy 1088 AACGTTTTCAGAAAGCTTTCTGTAATAATCTTCTGTAGAGAGCAATCCACGCCAC 1147
 Db 1088 AGGCTTTTCAAAAGCTTTCTGTAATAATTTGTATTAATAAGCAACCTCTACATCAC 1147
 Qy 1148 ACAACCG 1154
 Db 1148 AACACAG 1154
 RESULT 10
 AA167750
 ID AA167750 standard, cDNA, 1173 BP.
 AC AA167750;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Human histamine H4 receptor protein encoding cDNA.
 XX
 KM Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive;
 KM antidiabetic; antiallergic; neuroprotective; antidiabetic; human;
 KM cerebroprotective; cAMP modulator; gene therapy; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1173
 FT /tag= a
 FT /product= "histamine H4 receptor"
 XX
 PN W0200185786-A2.
 PD 15-NOV-2001.
 XX
 PF 04-MAY-2001; 2001MO-US014527.
 XX
 PR 05-MAY-2000; 2000US-0202151P.
 PR 23-AUG-2000; 2000US-0227567P.
 PR 13-NOV-2000; 2000US-0247855P.
 XX
 PA (AMHP) AMERICAN HOME PROD CORP.
 PI Jones PG, Blatcher M, Wu S, Pausch MH;
 XX WPI: 2002-049442/06.
 DR P-PSDB; AAG66023.
 XX
 PT New histamine receptor, termed H4 useful for detecting H4 (ant)agonists
 PT for treating transplanted organ rejection, asthma, allergy, multiple
 PT sclerosis and rheumatoid arthritis.
 XX

PS Claim 13; Fig 1; 66pp; English.
 XX
 CC The invention provides an isolated histamine receptor, H4, which binds
 CC ligands comprising imidazole attached to amine by an alkyl chain. The H4
 CC receptor can be expressed by standard recombinant methodology. Cells
 CC expressing H4 receptor protein at a detectable level can suppress cyclic
 CC adenosine monophosphate (cAMP) formation when contacted with the H4
 CC receptor agonist. The H4 receptor and antibodies are used for identifying
 CC H4 receptor modulators. Modulation of histamine H4 receptors is useful
 CC for treating transplanted organ rejection, asthma, allergies and
 CC autoimmune pathologies such as multiple sclerosis, type I diabetes,
 CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor
 CC protein and nucleic acids are useful targets to identify drugs that are
 CC effective in treating disorders associated with histamine-regulated
 CC processes. Identification and isolation of H4 receptor provides for
 CC development of screening of molecules that interact with H4 receptors.
 CC Genetic variants of H4 can be used to diagnose an H4 associated disease
 CC as described above. The H4 receptor polynucleotide is useful to treat or
 CC prevent a disorder associated with the function of H4 in peripheral blood
 CC leukocytes. The present sequence represents a cDNA encoding the human
 CC histamine H4 receptor protein
 XX
 SQ Sequence 1173 BP; 296 A; 245 C; 231 G; 401 T; 0 U; 0 Other;
 Query Match 57.7%; Score 675; DB 6; Length 1173;
 Best Local Similarity 74.9%; Pred. No. 3,5e-190;
 Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;
 Qy 8 CAAATACAGTACATGCGCTTAACTCAATTAATAATTTCTTGTACATTTTAATGCTT 67
 Db 11 CTATATGACAAATCAATTAATTAATCACTAGACATCGTGTACTTATGATTTTATGTCTT 70
 Qy 68 TACTACTATGCTATTAATGTTAGCAATGCTGTGCTATTTAGTTTATTTATGTAGCA 127
 Db 71 TAGTACTCTTGTCTAATAATGCTAGAAATGCTTGTGCTATTTAGCTTTTGTGTAGCA 130
 Qy 128 GAAATCTTACAGACATCAAGTAATTAATCTTTTCTTAACTTGGCCATTTGAGACTTCTTG 187
 Db 131 AAAACCTTACAGACATCAAGTAATTAATCTTTTCTTAACTTGGCCATTTGAGACTTCTTG 190
 Qy 188 TGGGTGCAATTTGCAATTTCTGTGACATACCTTCTGTGACTTACGTGACTTTGTGAA 247
 Db 191 TGGGTGCAATTTGCAATTTCTGTGACATACCTTCTGTGACTTACGTGACTTTGTGAA 250
 Qy 248 AGCAAGCTTGTGATTTTGGCTATTAATGACTATCTTTTATTAATGACATCTGTGATA 307
 Db 251 AGCAAGCTTGTGATTTTGGCTATTAATGACTATCTTTTATTAATGACATCTGTGATA 310
 Qy 308 ATATTGCTCATCAGCTAGATCGCTACAGCTCAAGTCAAAATGCGTGTGTATAGAG 367
 Db 311 ACATTTCTCATCAGCTAGATCGCTACAGCTCAAGTCAAAATGCGTGTGTATAGAG 370
 Qy 368 CTCAGCACTTGTGACCTGTGAAATTTGCTAATGCTGATGCTGTTGTGATATTTCTCT 427
 Db 371 CTCACATACCTGTGGGCTTGAAGATTGTTACTGTATGAGTGCGCGTGTGCTGCGCT 430
 Qy 428 TCATGCAAAATGGGCGGATGATTTCTGATTTCAAGCTTTGGCAGATTAAGCACTACGAAT 487
 Db 431 TCTTAGTGAATGGGCGGATGATTTCTGATTTCAAGCTTTGGCAGATTAAGCACTACGAAT 490
 Qy 488 GTGAACCTGATTTTAAAGTGTGACTTTGCTCTCCCTACATCATATTATTTGAATTC 547
 Db 491 GTGAACCTGATTTTAAAGTGTGACTTTGCTCTCCCTACATCATATTATTTGAATTC 550
 Qy 548 TGATCCCATCTTGTAGTGTCTTATTTCAAGCGCCCATATTTAATGAGCTGTGAAAGC 607
 Db 551 TGATCCCATCTTGTAGTGTCTTATTTCAAGCGCCCATATTTAATGAGCTGTGAAAGC 610
 Qy 608 GAGAGAAATGAGCAGCTGCTACAGCACTCTATCTCCCTGTGACTCTTTCAGCAGTG 667
 Db 611 GTGATATCTCTAGTATGAGTGTGCAAGGCAATCTGAGATGACTGTGTCTTTCACACA 667
 Qy 668 ACCAGGACACTCTCTGACAGACAGACCCGATTCAGAGGCACTGTGCCAGCAGGAAG 727


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Db 491 GTGAACCTGATTTTTTGGAAATGATCCTTGGCATCATATCTTGGAAATTCG 550
Qy 548 TGAATCCCATCTTGTATGTTGCTTATTTGAGCCCATATTTATCTGAGCCTTGAAAC 607
Db 551 TGAATCCCATCTTGTATGTTGCTTATTTGAGCCCATATTTATCTGAGCCTTGAAAC 610
Qy 608 GAGAGAACTGAGCAGGTGCTCAGCAGCCCTGATCCCTGATCTCTTCCAGCAGTG 667
Db 611 GTGATCATCTCATAGTAGTGGCCAAAGCCATCTGAGCTGCTGTCTTCCAAACA--- 667
Qy 668 ACCAGCAGACCTCTGAGACAGAACCCGATTTCAAGGGGAGCTTCCAGCAGCAGAAAG 727
Db 668 TCTGTGAGACCTCATTCAGAGGTATGATATCTTCAAGAGATCTCTTTCGATCGACAG 727
Qy 728 AAACAACTGCTCTCTTGGTTCAGACAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 787
Db 728 AAGTTCCTGATCTTTCATTTCAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787
Qy 788 TAAGAGCTTCAAGAAACAGCAATGTGATGCTTCAAAATGGGCTTCTCCCACTCAG 847
Db 788 CAGAAACAGAGATGATAGCAATATCAATTTGCTTCAAAATGGGCTTCTTCCCAATCAG 847
Qy 848 ATTCCCTGCTCTTTCAGCAAAAGGAAACATATCGAACTTTTCAGAGCCAGAGAAATTAAGCA 907
Db 848 ATTCTGATCTTTCACCAAAAGGAAACATATGTAAGTCTTTCAGAGCCAGAGATTAAGCA 907
Qy 908 AGTCACTGGGCAATCTTTCAGCAAAAGGAAACATATGTAAGTCTTTCAGAGCCAGAGAT 967
Db 908 AGTCACTGGGCAATCTTTCAGCAAAAGGAAACATATGTAAGTCTTTCAGAGCCAGAGAT 967
Qy 968 CAGTTATCTACTATTTTCTGAAAGAACTGATTAATCACTGATTAATCACTGATTAATCA 1027
Db 968 CAGTTATCTACTATTTTCTGAAAGAACTGATTAATCACTGATTAATCACTGATTAATCA 1027
Qy 1028 CTTTTCCTGCTCAGTGGTTCATTTCTTGTATCCCTTTTGTATCCATTTGATGATGATG 1087
Db 1028 CATTTCCTGCTCAGTGGTTCATTTCTTGTATCCCTTTTGTATCCATTTGATGATGATG 1087
Qy 1088 AAGCTTTTCAGAAAGGCTTCTGTAATAATCTTCTGTGAGAGAGCAATCCAGCCACAC 1147
Db 1088 AAGCTTTTCAGAAAGGCTTCTGTAATAATCTTCTGTGAGAGAGCAATCCAGCCACAC 1147
Qy 1148 ACAACCG 1154
Db 1148 AACACAG 1154

RESULT 12
ADG98759
ID ADG98759 standard; cDNA; 1173 BP.
XX
AC ADG98759;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human orphan GPCR cDNA, RUP7.
XX
KW Human; G protein-coupled receptor; GPCR; research tool; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1173
FT /tag= a
FT /product= "Human GPCR protein"
XX
PN US2003148450-A1.
XX
PD 07-AUG-2003.
XX
PF 17-OCT-2002; 2002US-00272983.
XX

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PR 20-NOV-1998; 98US-0109213P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123949P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0136567P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-0141448P.
PR 28-SEP-1999; 99US-0156333P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156634P.
PR 12-OCT-1999; 99US-00417044.
XX
PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LIAM/) LIAM C W.
PA (LINI/) LIN I.
XX
PI Chen R, Dang HT, Liam CW, Lin I;
XX
DR WPI; 2003-897571/82.
XX
DR P-PDB; ADG98760.
XX
PT New cDNA encoding a human G protein coupled receptor, useful for making a
PT probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR
PT identification of the expression of the receptor in tissue samples.
XX
PS Claim 25; SEQ ID NO 13; 52bp; English.
XX
CC The present invention provides novel human G protein-coupled receptor
CC (GPCR) proteins and their encoding nucleic acids. The invention is useful
CC for making a probe for dot-blot analysis and for RT-PCR identification of
CC the expression of the receptor in tissue samples. The invention is also
CC useful for identifying candidate compounds as inverse agonists, agonists
CC or partial agonists and as research tools in determining the location of
CC the receptors within the body. The present sequence is human orphan G
CC protein-coupled receptor cDNA.
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 57.7%; Score 675; DB 10; Length 1173;
Best Local Similarity 74.9%; Pred. No. 3, 5e-190;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAATATACAGTACATCGCCTTAACATCAATTAATTTCTTGAATTTTATGCTT 67
Db 11 CTAAATGACACATCAATTTATCTAAGCAGCTGCTTACTTATGATTTTATGCTT 70
Qy 68 TACTAGCTATGCTATTAATGTTAGCAATGTCGTGTCATTTTATGTTATGAGCA 127
Db 71 TAGTACCTTTTGTCTATTAATGCTAGAAATGCTTGTGTCATTTTATGCTTATG 130
Qy 128 GAATCTTACACATCGAAGTATTAATTTTCTTAACTTGGCCATTTGAGCATTTCT 187
Db 131 AAACCTTACACATCGAAGTATTAATTTTCTTAACTTGGCCATTTGAGCATTTCT 190
Qy 188 TGGTGCAATTTGCAATTTCTGTATACACTTCTGTGATCTTGTGACTTGTGAA 247
Db 191 TGGGTGATCTTCATTTCTTGTATACCTCTCACAGCGCTTTCGATGAGATTTTGA 250
Qy 248 AGCAAGCTGTGATTTTGGCTCATTAAGTATCTTTTATGATGAGATCTGTGATA 307
Db 251 AGAAATCTGTGATTTTGGCTCATTAAGTATCTTTTATGATGAGATCTGTGATA 310
Qy 308 ATATGCTTCATCACTAGATGATGCTTACAGTATGATGATGATGATGATGATG 367
Db 311 ACATGCTTCATCACTAGATGATGATGATGATGATGATGATGATGATGATGATG 370
Qy 368 CTCAGCACTTGGCAGCTGGAATTAATGCTACTAGATGATGATGATGATGATGCT 427

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Db 371 CTCAACATACCTGGGCTTGAAGATTGTACTGTAGTGCGCCCTTGGGCTGGCCCT 430
 Qy 428 TCATGACAAATGGGCGATGATTCGATTTCAGACTCTTGGAGAAATGCACTACAGAT 487
 Db 431 TCTTAGTGAATGGGCGATGATTCGATTTCAGACTCTTGGAGAAATGCACTACAGAT 490
 Qy 488 GTGAACCTGGATTTTAAAGAGTACTTGTCTCTCCCTCATCATATTGAATTC 547
 Db 491 GTGAACCTGGATTTTAAAGAGTACTTGTCTCTCCCTCATCATATTGAATTC 550
 Qy 548 TGAATCCCATCTTTGATGCTTATTTAGAGCCCATTTACTGAGCCTGTGGAAGC 607
 Db 551 TGATCCCATCTTTGATGCTTATTTAGAGCCCATTTACTGAGCCTGTGGAAGC 610
 Qy 608 GAGAGAACTGAGAGGCTGCTGAGCACCCTGTACTCCCTCTGATCTTCAGAGAG 667
 Db 611 GTGATCATCTCAGTGTGAGTCCAAAGCCATCTGAGTACTGCTCTCTTCCAAAC 667
 Qy 668 ACCAGGACACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727
 Db 668 TCTGTGAGACACTCATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727
 Qy 728 AAACAACTGCTCTCTGCTTGTGATGACAGAGTCAAGAGAGAGAGAGAGAGAG 787
 Db 728 AAGTCTGAGACACTCTTGTGATGACAGAGTCAAGAGAGAGAGAGAGAGAGAG 787
 Qy 788 TAAAGAGCTCAAG 847
 Db 788 CAAAGAGCTCAAG 847
 Qy 848 ATTCCCTGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
 Db 848 ATTCTGTAGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
 Qy 908 AGTCACTGGCCATCTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 967
 Db 908 AGTCACTGGCCATCTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 967
 Qy 968 CAGTATCTACATCTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027
 Db 968 CAGTATCTACATCTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027
 Qy 1028 CCTTTGGCTCAG 1087
 Db 1028 CATTGTGGCTCAG 1087
 Qy 1088 AACCTTTTCAAG 1147
 Db 1088 AGCGCTTCAAG 1147
 Qy 1148 ACAACCG 1154
 Db 1148 AACACAG 1154

RESULT 13
 ID ABS57063 standard; cDNA; 1173 BP.
 XX ABS57063;

XX 28-JAN-2003 (fixed entry)

DE Human cDNA encoding G-protein coupled receptor AXOR35.

XX Human, ss; gene; G-protein coupled receptor; AXOR35; lymphocyte;
 KM macrophage; eosinophil; neutrophil; infection; transplant rejection;
 KM gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;
 KM Crohn's disease; irritable bowel syndrome; vomiting; inflammation;
 KM atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;
 KM psoriasis; neurological disease; urinary retention; cardiovascular disease;
 KM myocardial infarction; hypotension; hypertension; pulmonary disorder;

KM chronic obstructive pulmonary disease; cough; renal disease;
 KM renal ischaemia; arteriosclerosis; atherosclerosis; psychosis;
 KM neurological disorder; migraine; anorexia; anxiety; schizophrenia;
 KM dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;
 KM graft versus host disease; osteoporosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT 1. 1173
 FT CDS /tag= a
 FT /product= "AXOR35"
 PN US2002137054-A1.
 XX 26-SEP-2002.
 PD 20-JUL-2001; 2001US-00910411.
 PF 02-NOV-1999; 99US-00431898.
 PR 03-FEB-2000; 2000US-00497790.
 PR 20-OCT-2000; 2000US-00693761.
 XX (SMK) SMITHKLINE BEECHAM CORP.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 PI Aubart KM, Bergema DJ, Fitzgerald L, Graybill TL, Li X;
 PI Michalovich D, Morrow DM, Zhu Y;
 DR WPI, 2003-074982/07.
 DR P-PSDB; ABG71960.
 XX Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for
 PT treating infections, gastrointestinal disorders, autoimmune disorders,
 PT urological diseases, cardiovascular diseases and cancer.
 PS Claim 2; Page 21-22; 24pp; English.

CC The invention relates to an isolated G-protein coupled receptor
 CC polypeptide, AXOR35, (and its homologues and variants) and its encoding
 CC polynucleotide (and its homologues, variants, complements and RNA
 CC equivalents). Also included are an anti-AXOR35 antibody, an AXOR35
 CC expression vector, producing a recombinant host cell by introducing the
 CC vector into a cell such that the host cell produces AXOR35, a membrane of
 CC the host cell expressing AXOR35, identifying/screening for agonists or
 CC antagonists of AXOR35 and inhibiting or promoting the function of
 CC lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,
 CC by administering to the patient AXOR35 agonists or antagonists. The
 CC agonist or antagonist identified is useful for treating a disease such as
 CC asthma, or for inhibiting or promoting the function of lymphocytes,
 CC macrophages, eosinophils, or neutrophils in diseased tissue such as an
 CC asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays,
 CC for identifying compounds that are agonists or antagonists of AXOR35, as
 CC vaccines, or for treating infections (bacterial, fungal, protozoan or
 CC viral infections), transplant rejection, gastrointestinal disorders (such
 CC as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),
 CC irritable bowel syndrome, vomiting, inflammation (such as atopic
 CC dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,
 CC psoriasis), urological diseases (such as urinary retention),
 CC cardiovascular diseases (such as myocardial infarction), hypotension,
 CC hypertension, pulmonary disorders (such as chronic obstructive pulmonary
 CC disease), cough, renal diseases (such as renal ischaemia),
 CC arteriosclerosis, atherosclerosis, psychotic and neurological disorders
 CC (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such
 CC as Parkinson's disease), cancer, obesity, stroke, septic shock, graft
 CC versus host disease and osteoporosis. The present sequence is the cDNA
 CC encoding AXOR35
 CC XX

SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 57.7%; Score 675; DB 10; Length 1173;
 Best Local Similarity 74.9%; Pred. No. 3.5e-190;
 Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAATAACAGTACGATGCGCTTAACATCAATTAATAATTTCTTGACATTTTAAATGCTT 67
 DB 11 CTATATGCAACAATCAATTTATCACTAGACACTGCTGTACTTTAGCATTTTATATGCTT 70
 QY 68 TACTAGCTATTTGCTTAATAGTTAGGCAATGTCGTGCTATTTAGCTTTTATTTGTGACA 127
 DB 71 TAGTACTTTTGTCTATATAGTCTAGAAATGCTTTGGTCATTTTAGCTTTTGTGTGACA 130
 QY 128 GAATCTTACATCCAGAAATTAATCTTTTCTTAATCTTGCGCATTTGACACTTCTTGG 187
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 ID ADJ26922 standard; cDNA; 1173 BP.
 AC ADJ26922;
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 DT 20-MAY-2004 (first entry)
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 DE Human endogenous orphan G-protein coupled receptor RUP7 cDNA.
 XX
 KW Human: G protein-coupled receptor; GPCR; dot-blot analysis;
 KW pharmaceutical agent; gene; ss.
 OS Homo sapiens.
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 FH Key Location/Qualifiers
 FT CDS 1..1173
 FT /+tag= a
 FT /product= "Human endogenous orphan GPCR protein"
 PN US2003175891-A1.
 PD 18-SEP-2003.
 XX
 PF 21-MAR-2003; 2003US-00393807.
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 PR 20-NOV-1998; 98US-0109213P.
 PR 16-FEB-1999; 99US-0120416P.
 PR 26-FEB-1999; 99US-0121852P.
 PR 12-MAR-1999; 99US-0123946P.
 PR 12-MAR-1999; 99US-0123949P.
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 PR 12-OCT-1999; 99US-00417044.
 PR 17-OCT-2002; 2002US-00272983.
 XX
 PA (CHEN/) CHEN R.
 PA (DANG/) DANG H T.
 PA (LIAM/) LIAM C W.
 PA (LIN/) LIN I.
 PI Chen R, Dang HT, Liam CW, Lin I;
 XX
 DR WPI; 2003-898539/82.
 DR P-PSDB; ADJ26923.
 XX
 PT New human G protein-coupled receptor and its coding cDNA, useful for
 PT disease or disorder identification and/or selection, for screening of
 PT candidate compounds useful as pharmaceutical agents, and in research
 PT applications.

XX Claim 25; SEQ ID NO 13; 53bp; English.

CC The present invention relates to human endogenous orphan G protein-
CC coupled receptor (GPCR) proteins and polynucleotides encoding such
CC proteins. The cDNA sequence of the human G protein-coupled receptor
CC (GPCR) is useful in making a probe for dot-blot analysis against tissue-
CC mRNA and/or for RT-PCR identification of the expression of the receptor
CC in tissue samples. GPCR sequences of the invention may be used in
CC disease/disorder identification and/or selection, in screening of
CC candidate compounds for use as pharmaceutical agents and in research
CC settings. The present sequence is human endogenous orphan GPCR cDNA.

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 57.7%; Score 675; DB 11; Length 1173;

Beet Local Similarity 74.9%; Pred No. 3.5e-190;

Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

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QY      968 CAGTATCTACTCATTTTCTTCTGAAAGAACTTGAATTAATCAACCTGTATCACTG 1027
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DB      1088 AGCGCTTCAAAAGGCTTTCTTGAATAATTTGTATAAAAAGCAACCTTACCATCAC 1147
QY      1148 ACAACCG 1154
DB      1148 AACACAG 1154
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RESULT 15

ADG86374 ID ADG86374 standard; cDNA, 1173 BP.

ADG86374;

11-MAR-2004 (first entry)

Human endogenous orphan GPCR hRUP7 cDNA.

Human; ss; gene; endogenous orphan GPCR; G protein-coupled receptor;

transmembrane domain 6.

Homo sapiens.

US2003229216-A1.

11-DEC-2003.

16-APR-2003; 2003US-00417820.

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PR      27-NOV-1998; 98US-0110060P.
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PR      26-FEB-1999; 98US-0121852P.
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PR 01-OCT-1999; 99US-0157280P.
 PR 01-OCT-1999; 99US-0157281P.
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 PR 12-OCT-1999; 99US-00416760.
 XX
 PA (CHEN/) CHEN R.
 PA (LIAM/) LIAM C. W.
 PA (LOWIT/) LOWITZ K.
 PA (CHAL/) CHALMERS D. T.
 PA (BEHA/) BEHAN D. P.
 PI Chen R, Liam CW, Lowitz K, Chalmers DT, Behan DP;
 XX
 DR WPI; 2004-052038/05.
 DR P-PSDB; ADG86375.
 PT New cDNA encoding a non-endogenous, constitutively activated version of a
 PT inverse or partial agonists having potential applicability as therapeutic
 PT agents.
 XX
 PS Example 1; SEQ ID NO 13; 110pp; English.
 XX

CC The invention relates to a cDNA encoding a non-endogenous, constitutively
 CC activated version of a human G protein-coupled receptor comprising hARE-
 CC 3(F313K), hARE-4(V233K), hARE-5(A240K), hGPCR14(L257K), hGPCR27(C283K),
 CC hARE-1(E232K), hARE-2(G285K), hEPRI (L239K), hG2A(K232A), hRUP3(L224K),
 CC hRUP5(A236K), hRUP6(N267K), hRUP7(A302K), hCHN4(V244K),
 CC hCHN5(S244K), hCHN6(L352K), hCHN8(N235K) or h9(F236K). Also included are
 CC a non-endogenous version of a human G protein-coupled receptor encoded by
 CC the cDNA, a plasmid comprising the vector and the cDNA and a host cell
 CC comprising the plasmid. The cDNA encodes a non-endogenous, constitutively
 CC activated version of a human G protein-coupled A71 receptor comprising
 CC the angiotensin II type 1 receptor hAT1(F239K), hAT1(N111A),
 CC hAT1(AT24551C3, a domain swap mutant) or hAT1(A243+). The mutation is of
 CC an amino acid 16 residues from the proline in transmembrane domain 6 and
 CC is usually to a lysine. The cDNA is useful for identifying candidate
 CC compounds as receptor agonists, inverse agonists or partial agonists
 CC having potential applicability as therapeutic agents. The present
 CC sequence is a cDNA (or fragment) for a wild-type human GPCR.
 CC
 XX

SO Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 57.7%; Score 675; DB 12; Length 1173;

Best Local Similarity 74.9%; Pred. No. 3.5e-190;

Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAATATACAGTACCAATGCGCTTAACATCAATTAATAATTTCTTGACATTTTAAATGCTT 67
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3	1170	100.0	1170	21	US-10-626-398-7 Sequence 7, Appli
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27	671.8	57.4	1265	15	US-10-290-078-25 Sequence 25, Appli
28	616.8	52.7	1176	20	US-10-626-445-6 Sequence 6, Appli
29	616.8	52.7	1176	21	US-10-626-126-6 Sequence 6, Appli
30	616.8	52.7	1176	21	US-10-626-398-6 Sequence 6, Appli
31	613	52.4	1176	20	US-10-626-445-5 Sequence 5, Appli
32	613	52.4	1176	21	US-10-626-126-5 Sequence 5, Appli
33	613	52.4	1176	21	US-10-626-398-5 Sequence 5, Appli
34	270	23.1	1326	19	US-10-398-036-19 Sequence 19, Appli
35	155.4	13.3	1223	19	US-10-283-975A-637 Sequence 697, App
36	132.2	11.3	1239	9	US-09-891-053-2 Sequence 2, Appli
37	132.2	11.3	1239	21	US-10-759-463-2 Sequence 2, Appli
38	132.2	11.3	2700	9	US-09-891-053-5 Sequence 5, Appli
39	132.2	11.3	2700	21	US-10-759-463-5 Sequence 5, Appli
40	124.2	10.6	1311	22	US-10-495-676A-7 Sequence 7, Appli
41	123	10.5	1338	9	US-09-350-206-6 Sequence 6, Appli
42	123	10.5	1338	9	US-09-349-755-6 Sequence 6, Appli
43	123	10.5	1338	9	US-09-166-334-6 Sequence 6, Appli
44	123	10.5	1338	15	US-10-282-958-6 Sequence 6, Appli
45	123	10.5	1953	9	US-09-891-053-26 Sequence 26, Appli

ALIGNMENTS

RESULT 1
US-10-626-445-7
; Sequence 7, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OR INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PBD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Cavia porcellus
US-10-626-445-7

Query Match 100.0%; Score 1170; DB 20; Length 1170;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGCAATAAAGTACATGCGCTTAACATCAATTAATTTCTTGACATTTTGA 60
Db 1 ATGTGGCAATAAAGTACATGCGCTTAACATCAATTAATTTCTTGACATTTTGA 60

QY 61 ATGCTTTACTAGCTATGCTATTAATGTTAGGCAATGCTGCTGATTTTACTTTTAT 120
DB 61 ATGCTTTACTAGCTATGCTATTAATGTTAGGCAATGCTGCTGATTTTACTTTTAT 120
QY 121 GTGGACAGAAATCTTGAAGATGAAGTAACTTTTCTTAACTTGGCCCTTGACAC 180
DB 121 GTGGACAGAAATCTTGAAGATGAAGTAACTTTTCTTAACTTGGCCCTTGACAC 180
QY 181 TTCTTTGGGGGTGCAATTCCTCTGTACATACCTCTCCGCTGACTTACTGACT 240
DB 181 TTCTTTGGGGGTGCAATTCCTCTGTACATACCTCTCCGCTGACTTACTGACT 240
QY 241 TCTGAAAGCAAGCTTGTGTATTTTGGCTCATTTACTGACTATCTTTTATGACAGACT 300
DB 241 TCTGAAAGCAAGCTTGTGTATTTTGGCTCATTTACTGACTATCTTTTATGACAGACT 300
QY 301 GTGTATTAATTTGTCTCTACAGTACGATGCTGACAGTCTCAAAATCCGTGTG 360
DB 301 GTGTATTAATTTGTCTCTACAGTACGATGCTGACAGTCTCAAAATCCGTGTG 360
QY 361 TATAGAGCTCAGACACTCTGGAAGCTGGAATTTGCTACTCAGATGCTGCTTTGATA 420
DB 361 TATAGAGCTCAGACACTCTGGAAGCTGGAATTTGCTACTCAGATGCTGCTTTGATA 420
QY 421 TTCTCTTCATGACAAATGGGCGGATGATTTGATTTGACACTCTTGGCAATAGACT 480
DB 421 TTCTCTTCATGACAAATGGGCGGATGATTTGATTTGACACTCTTGGCAATAGACT 480
QY 481 ACAGAAATGGAACCTTGATTTTAAAAAGGTGACTTTGCTCTCCCTCATCATTTATG 540
DB 481 ACAGAAATGGAACCTTGATTTTAAAAAGGTGACTTTGCTCTCCCTCATCATTTATG 540
QY 541 GAATTCCTGATCCCATCTTGTAGTGTCTTATTTTCAAGGCGCCATATTACTGAGCCTG 600
DB 541 GAATTCCTGATCCCATCTTGTAGTGTCTTATTTTCAAGGCGCCATATTACTGAGCCTG 600
QY 601 TGGAAAGCGAGAAACCTGAGAGGTGCTCAGCCACCTCTGATCTCCCTCTGACTTTC 660
DB 601 TGGAAAGCGAGAAACCTGAGAGGTGCTCAGCCACCTCTGATCTCCCTCTGACTTTC 660
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DB 661 AGCAATGACAGGACACTCTCTGACAGACAGAACCCGATTTCAAGGGCGACTCTTGAC 720
QY 721 CGGAAAGAAACAACTGCTCTCTTGGTTCAGACAGTCAAGGAGAGAGAGAGTCTTGG 780
DB 721 CGGAAAGAAACAACTGCTCTCTTGGTTCAGACAGTCAAGGAGAGAGAGAGTCTTGG 780
QY 781 TTTTCCATTAAGAGCTTACAAAGACAGCAATGTATGCTTCCAAATGGGCTTCTCTCC 840
DB 781 TTTTCCATTAAGAGCTTACAAAGACAGCAATGTATGCTTCCAAATGGGCTTCTCTCC 840
QY 841 CACTCAGATTCCTGCTGCTTTCAGCAAGGAGAAATATGAACTTTTCAGAGCCAGAA 900
DB 841 CACTCAGATTCCTGCTGCTTTCAGCAAGGAGAAATATGAACTTTTCAGAGCCAGAA 900
QY 901 TTAGCAAGTCACTGAGGCTTCTTGAAGCTTTTGGCAATTTGGCTGCTCATATTTCA 960
DB 901 TTAGCAAGTCACTGAGGCTTCTTGAAGCTTTTGGCAATTTGGCTGCTCATATTTCA 960
QY 961 CTGACTACAGTATCTACTCAATTTTCTTGAAGGAACTTGAATCAACTGTGTAC 1020
DB 961 CTGACTACAGTATCTACTCAATTTTCTTGAAGGAACTTGAATCAACTGTGTAC 1020
QY 1021 CATACTGCTTTTGGCTCAGAGGTTCATTTCTTTGTAATCCCTTTTGTATGATTTG 1080
DB 1021 CATACTGCTTTTGGCTCAGAGGTTCATTTCTTTGTAATCCCTTTTGTATGATTTG 1080
QY 1081 TGTCAAAAGCTTTTCAAGAGGCTTCTGAAATATCTCTGTGAGAGGCAATCCAG 1140
DB 1081 TGTCAAAAGCTTTTCAAGAGGCTTCTGAAATATCTCTGTGAGAGGCAATCCAG 1140

QY 1141 CCACCACAAACCGCTCAATATCCACTTGA 1170
DB 1141 CCACCACAAACCGCTCAATATCCACTTGA 1170
RESULT 2
US-10-626-126-7
; Sequence 7, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: *Cavia porcellus*
US-10-626-126-7
Query Match 100.0%; Score 1170; DB 21; Length 1170;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTTGGCAATTAACAGTACAAATCCCTTAACATCAATTAATTTCTTGGACATTTTAA 60
DB 1 ATGTTGGCAATTAACAGTACAAATCCCTTAACATCAATTAATTTCTTGGACATTTTAA 60
QY 61 ATGCTTTACTAGCTATGCTATTAATGTTAGGCAATGCTGCTGATTTTACTTTTAT 120
DB 61 ATGCTTTACTAGCTATGCTATTAATGTTAGGCAATGCTGCTGATTTTACTTTTAT 120
QY 121 GTGGACAGAAATCTTGAAGATGAAGTAACTTTTCTTAACTTGGCCCTTGACAC 180
DB 121 GTGGACAGAAATCTTGAAGATGAAGTAACTTTTCTTAACTTGGCCCTTGACAC 180
QY 181 TTCTTTGGGGGTGCAATTCCTCTGTACATACCTCTCCGCTGACTTACTGACT 240
DB 181 TTCTTTGGGGGTGCAATTCCTCTGTACATACCTCTCCGCTGACTTACTGACT 240
QY 241 TCTGAAAGCAAGCTTGTGTATTTTGGCTCATTTACTGACTATCTTTTATGACAGACT 300
DB 241 TCTGAAAGCAAGCTTGTGTATTTTGGCTCATTTACTGACTATCTTTTATGACAGACT 300
QY 301 GTGTATTAATTTGTCTCTACAGTACGATGCTGACAGTCTCAAAATCCGTGTG 360
DB 301 GTGTATTAATTTGTCTCTACAGTACGATGCTGACAGTCTCAAAATCCGTGTG 360
QY 361 TATAGAGCTCAGACACTCTGGAAGCTGGAATTTGCTACTCAGATGCTGCTTTGATA 420
DB 361 TATAGAGCTCAGACACTCTGGAAGCTGGAATTTGCTACTCAGATGCTGCTTTGATA 420
QY 421 TTCTCTTCATGACAAATGGGCGGATGATTTGATTTGACACTCTTGGCAATAGACT 480
DB 421 TTCTCTTCATGACAAATGGGCGGATGATTTGATTTGACACTCTTGGCAATAGACT 480
QY 481 ACAGAAATGGAACCTTGATTTTAAAAAGGTGACTTTGCTCTCCCTCATCATTTATG 540
DB 481 ACAGAAATGGAACCTTGATTTTAAAAAGGTGACTTTGCTCTCCCTCATCATTTATG 540
QY 541 GAATTCCTGATCCCATCTTGTAGTGTCTTATTTTCAAGGCGCCATATTACTGAGCCTG 600
DB 541 GAATTCCTGATCCCATCTTGTAGTGTCTTATTTTCAAGGCGCCATATTACTGAGCCTG 600
QY 601 TGGAAAGCGAGAAACCTGAGAGGTGCTCAGCCACCTCTGATCTCCCTCTGACTTTC 660

Db 601 TGGAAAGAGAGAACTGAGCAGGTGCTCAGCCACCTGTACTCCCTCTGACTCTTCC 660
Qy 661 AGAAGTACACGAGACATCTCTGACAGAGACCCGATTCAGGGGAGATCTGCCAGCA 720
Db 661 AGAAGTACACGAGACATCTCTGACAGAGACCCGATTCAGGGGAGATCTGCCAGCA 720
Qy 721 CGGAAAGAAACAACCTGCTCTCTTGGTTCAGACAGTCAAGAGAAAGACAGTCTTTC 780
Db 721 CGGAAAGAAACAACCTGCTCTCTTGGTTCAGACAGTCAAGAGAAAGACAGTCTTTC 780
Qy 781 TTTTCCATAAGAGCTTACAAAGAACAGCAATGTATGCTTCCAAAATGGGCTTCTCTCC 840
Db 781 TTTTCCATAAGAGCTTACAAAGAACAGCAATGTATGCTTCCAAAATGGGCTTCTCTCC 840
Qy 841 CACTCAGATTCCTGGCTCTTTCAGCAAGAGGAAACATATGCACTTTTCAGAGCAGAGAA 900
Db 841 CACTCAGATTCCTGGCTCTTTCAGCAAGAGGAAACATATGCACTTTTCAGAGCAGAGAA 900
Qy 901 TTAGCCAGTCACTGGGCAATCTTATAGCAGCTTTTGCCATTTGGGCTGCTCATATTC 960
Db 901 TTAGCCAGTCACTGGGCAATCTTATAGCAGCTTTTGCCATTTGGGCTGCTCATATTC 960
Qy 961 CTGACTACAGTTATCTACTCATTTTTCCTGAAAGAACTTGAATAATCAACTGTATC 1020
Db 961 CTGACTACAGTTATCTACTCATTTTTCCTGAAAGAACTTGAATAATCAACTGTATC 1020
Qy 1021 CATACGCTCTTTGGCTCCAGGTGTCATCTCTTTGTTATATCCCTTTTGTATTCATTG 1080
Db 1021 CATACGCTCTTTGGCTCCAGGTGTCATCTCTTTGTTATATCCCTTTTGTATTCATTG 1080
Qy 1081 TGTCAAAAAGCTTTTTCAGAAAGGCTTCTGAAATACTTCTGTGAGAGGCAATCCAG 1140
Db 1081 TGTCAAAAAGCTTTTTCAGAAAGGCTTCTGAAATACTTCTGTGAGAGGCAATCCAG 1140
Qy 1141 CCACCAACACCGCTCAATATCCACTTGA 1170
Db 1141 CCACCAACACCGCTCAATATCCACTTGA 1170

RESULT 3
US-10-626-398-7
; Sequence 7, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovemberg, Timothy
; APPLICANT: Liu, Changli
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Cavia porcellus
US-10-626-398-7

Query Match 100.0%; Score 1170; DB 21; Length 1170;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGGCAAAATTAACAGTACATCGCTTAACATCAATTAATTTCTTTGACATTTTGA 60
Db 1 ATGTGGCAAAATTAACAGTACATCGCTTAACATCAATTAATTTCTTTGACATTTTGA 60
Qy 61 ATGTCTTACTAGCTATTTGCTATATGTTAGGCAATGCTGTGCAATTTAGCTTTTAT 120
Db 61 ATGTCTTACTAGCTATTTGCTATATGTTAGGCAATGCTGTGCAATTTAGCTTTTAT 120

Db 61 ATGTCTTACTAGCTATTTGCTATATGTTAGGCAATGCTGTGCAATTTAGCTTTTAT 120
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Db 121 GTGACAGAAATTTTGAATCGAAGTAATTAATTTTCTTAACTTGGCATTGGAC 180
Qy 181 TTCTTTGGGTGCAATTCGCAATTCCTGTATACATACCTTCTGTGATTAAGTACTG 240
Db 181 TTCTTTGGGTGCAATTCGCAATTCCTGTATACATACCTTCTGTGATTAAGTACTG 240
Qy 241 TCTGAAAGCAAGCTTGTATTTTGGCTCATTAAGTACTGATATCTTTTATAGACATCT 300
Db 241 TCTGAAAGCAAGCTTGTATTTTGGCTCATTAAGTACTGATATCTTTTATAGACATCT 300
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Db 301 GTGTATTAATTTTCTTCAATCACTACAGTACAGTACAGTACAGTACAGTACAGTAC 360
Qy 361 TATAGAGCTCAGCACTCTGGCACTTGAAATTTGCTACTAGATGGTGGCTGTTGGATA 420
Db 361 TATAGAGCTCAGCACTCTGGCACTTGAAATTTGCTACTAGATGGTGGCTGTTGGATA 420
Qy 421 TTCTCTTCAATGCAAAATGGGCGGATGATTTGATTTCAAGCTTTGGCAATAGCACT 480
Db 421 TTCTCTTCAATGCAAAATGGGCGGATGATTTGATTTCAAGCTTTGGCAATAGCACT 480
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Db 481 ACAGAAATGGAACCTGATTTTAAAGTGTGATCTTGTCTCTCCATATCATATTG 540
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Db 541 GAATTCCTGATCCCATCTTGTAGTGTGCTTATTTAGCGGCCCATATTTACTGAGCTG 600
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Db 661 AGCAGTACACGAGACATCTCTGACAGAGAGACCCGATTCAGGGGAGATCTGCCAGCA 720
Qy 721 CGGAAAGAAACAACCTGCTCTCTTGGTTCAGACAGTCAAGAGAAAGACAGTCTTTC 780
Db 721 CGGAAAGAAACAACCTGCTCTCTTGGTTCAGACAGTCAAGAGAAAGACAGTCTTTC 780
Qy 781 TTTTCCATAAGAGCTTACAAAGAACAGCAATGTATGCTTCCAAAATGGGCTTCTCTCC 840
Db 781 TTTTCCATAAGAGCTTACAAAGAACAGCAATGTATGCTTCCAAAATGGGCTTCTCTCC 840
Qy 841 CACTCAGATTCCTGGCTCTTTCAGCAAGAGGAAACATATGCACTTTTCAGAGCAGAGAA 900
Db 841 CACTCAGATTCCTGGCTCTTTCAGCAAGAGGAAACATATGCACTTTTCAGAGCAGAGAA 900
Qy 901 TTAGCCAGTCACTGGGCAATCTTATAGCAGCTTTTGCCATTTGGGCTGCTCATATTC 960
Db 901 TTAGCCAGTCACTGGGCAATCTTATAGCAGCTTTTGCCATTTGGGCTGCTCATATTC 960
Qy 961 CTGACTACAGTTATCTACTCATTTTTCCTGAAAGAACTTGAATAATCAACTGTATC 1020
Db 961 CTGACTACAGTTATCTACTCATTTTTCCTGAAAGAACTTGAATAATCAACTGTATC 1020
Qy 1021 CATACGCTCTTTGGCTCCAGGTGTCATCTCTTTGTTATATCCCTTTTGTATTCATTG 1080
Db 1021 CATACGCTCTTTGGCTCCAGGTGTCATCTCTTTGTTATATCCCTTTTGTATTCATTG 1080
Qy 1081 TGTCAAAAAGCTTTTTCAGAAAGGCTTCTGAAATACTTCTGTGAGAGGCAATCCAG 1140
Db 1081 TGTCAAAAAGCTTTTTCAGAAAGGCTTCTGAAATACTTCTGTGAGAGGCAATCCAG 1140
Qy 1141 CCACCAACACCGCTCAATATCCACTTGA 1170
Db 1141 CCACCAACACCGCTCAATATCCACTTGA 1170

RESULT 4
 US-09-812-216-1
 ; Sequence 1, Application US/09812216
 ; Patent No. US20020098539A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Jiang Xu
 ; APPLICANT: Hedrick, Joseph A.
 ; APPLICANT: Laz, Thomas M.
 ; APPLICANT: Monsema, Frederick J. Jr.
 ; APPLICANT: Morse, Kelley L.
 ; APPLICANT: Umland, Shelby P.
 ; APPLICANT: Wang, Suke
 ; TITLE OF INVENTION: Histamine receptor
 ; FILE REFERENCE: CNO1069
 ; CURRENT APPLICATION NUMBER: US/09/812,216
 ; PRIOR FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: 09/414,010
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-812-216-1

Query Match 57.7%; Score 675; DB 9; Length 1173;
 Best Local Similarity 74.9%; Pred. No. 5,9e-185;

Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATACAGTAAATCGCTTACATCAATTAATTTCTTGAACATTTTAATGCTT 67
 DB 11 CTAATAGACATCAATTATCATAGACGCGTTACTTTAGCATTTTATGCTCT 70
 QY 68 TACTAGCTATTCCTTAATGTTAGGCAATGCTGCTCATTTTATTTATGAGACA 127
 DB 71 TAGTAGCTTTTCTTAATGCTTAAGGAAATGCTTGGTCAATTTTGTGAGACA 130
 QY 128 GAAATCTTAGACATGAGTAATTAATTTTCTTAACTTGGCAATGAGACTTCTTG 187
 DB 131 AAAACCTTAGACATGAGTAATTTTCTTAACTTGGCAATGAGACTTCTTG 190
 QY 188 TGGGTGCAATTCCTCTGTCATACCTTCTGCTGAGCTTACTGAGACTTCTGGA 247
 DB 191 TGGGTGTCATCCATTCCTTGTACATCCCTACACGCTGTGCAATGAGACTTCTGGA 250
 QY 248 AGCAAGCTTGTATTTTGGCTCATCTGACTATCTTTTATGTCAGCATCTGTGTATA 307
 DB 251 AGGAATCTGTATTTTGGCTCATCTGACTATCTTTTATGTCAGCATCTGTGTATA 310
 QY 308 ATATTGCTCATGCTCATGCTACAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG 367
 DB 311 ACATTGCTCATGCTCATGCTACAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG 370
 QY 368 CTCAGCACTTGGCACTGGAATTTGCTACTCAATGCTGCTGTTGATATTTCTCT 427
 DB 371 CTCACATCTGCGGCTTGAAGATTTGTAATCTGATGCTGCGCTTGGGCTGCGCT 430
 QY 428 TCATGACAAATGGCGGATGATTTGATTTGACACTTTGGCAGAAATAGCATACAAAT 487
 DB 431 TCTTAGTAAATGGCGCAATGATTTGATTTGACAGCTTGGGAGGATGAAATAGAT 490
 QY 488 GTGAACCTGAGTTTTTAAAGAGTGTACTTCTCTCCATCATCATTAATGGAATCC 547
 DB 491 GTGAACCTGAGTTTTTGGGATGATGATCTTGGCAATCATCATTAATGGAATTCG 550
 QY 548 TGATCCCATCTTTTGTAGTCTTATTTTCAGCGCCCATTTTACTGAGACTGTTGGAAGC 607
 DB 551 TGATCCCATCTTTTGTAGTCTTATTTTCAACATGAAATTTTATGAGACTGTTGGAAGC 610
 QY 608 GAGAGAACTGAGCAGGTGCTCAGCCACCTGTAATCCCTCTGACTCTTCCAGCAGTG 667

DB 611 GTGATCATCTCAGTAGTGCCAAAGCCATCTGAGCTAATGCTGTCTTCTTCAACA--- 667
 QY 668 ACCAGCACTCTCCGACAGAGACCCCGAATTCAGAGGCGCATCTGCGACAGCAAG 727
 DB 668 TCTGTGACACTCATTTCAAGAGTACATATCTTCAAGAGATCTTTTCTGTGATGACAG 727
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 DB 728 AAGTCTGATCTTTCATTCATTCAGAGACAGAGGAGAAAGATAGTCTCATGTTTCTCT 787
 QY 788 TAAAGCCTTAAAGAACGCAATGATGCTTCCAAATAGGCTTCTCTCCACTCAG 847
 DB 788 CAAGAACCAATGAAATGCAATCAATGCTTCCAAATAGGCTTCTCTCCACTCAG 847
 QY 848 ATTCCTGCTCTTCAAGAAAGGAAATGCAATCTTTCAGAGCCAGAAATAGCCA 907
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 QY 908 AGTCACTGGCAATCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 967
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 QY 968 CAGTATCTACTCATTTTCTGTAAGAAAGTCAATTAATCACTGTGACATACG 1027
 DB 968 CAATGCTCTTCAATTTATCTTCAAGCAAGCTTCAATTAATCACTGTGATAGATG 1027
 QY 1028 CTTTGGCTCAGAGTGTCAATCTTGTATTCCTTTTGTATTCATTTGTCATG 1087
 DB 1028 CATTTGGCTCAGAGTGTCAATCTTGTATTCCTTTTGTATTCATTTGTCATG 1087
 QY 1088 AACGTTTCAAGAGCTTTCAGAAATTAATCTTCTGTGAGAAAGCAATTCAGCCAGC 1147
 DB 1088 AGCGCTTCAAGAGCTTTCAGAAATTAATTTGTATTAAGAAAGCAATTCAGCATC 1147
 QY 1148 ACAACCG 1154
 DB 1148 AACACAG 1154

RESULT 5
 US-09-910-411-1
 ; Sequence 1, Application US/09910411
 ; Patent No. US20020137054A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bergsma, Derk
 ; APPLICANT: Fitzgerald, Laura
 ; APPLICANT: Li, Xiatong
 ; APPLICANT: Michalovich, David
 ; TITLE OF INVENTION: Axor35, A G-Protein Coupled Receptor
 ; FILE REFERENCE: GP70655-2C1
 ; CURRENT APPLICATION NUMBER: US/09/910,411
 ; PRIOR FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: 09/693,761
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 09/497,790
 ; PRIOR FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: 09/431,898
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-910-411-1

Query Match 57.7%; Score 675; DB 9; Length 1173;
 Best Local Similarity 74.9%; Pred. No. 5,9e-185;
 Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATACAGTAAATCGCTTACATCAATTAATTTCTTGAACATTTTAAATGCTT 67

11 CTAATGACAAATCAATTTATGCTAGAGCTGCTGTACTTATAGCATTTTATGCTCCT 70
68 TACTAGCTATTGTCTAATATGTTAGGCAATGCTGCTCATTTAGCTTTTATGTGACA 127
71 TAGTAGCTTTTGTATTAATGCTAGGAAAGCTTTGCTCATTTTATGCTTTTGTGTGACA 130
128 GAAATCTTAGACATGCAAGTAATTTACTTTTCTTAACTTGGCATTGAGACTTCTTG 187
131 AAAACCTTAGACATGCAAGTAATTTTCTTAACTTGGCATTGAGACTTCTTG 190
188 TGGGTGCAATGCAATTTCTGTACATACCTTCTGCTGACTTACGACTTCTGAA 247
191 TGGGTGCAATTTCTGCTTGTATCTTGTATCTTGTATCTTGTATCTTGTATCTTGTAT 250
248 AGCAAGCTTGTATTTTGGCTCATCTAGACTATCTTTATGTATACAGACTGTGTATA 307
251 AGGAAATCTGTATTTTGGCTCATCTAGACTATCTTTATGTATACAGACTGTGTATA 310
308 ATATTGCTCATCTAGACTATCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367
311 ACATTGCTCATCTAGACTATCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370
368 CTCAGACTCTGAGCACTGGAATTTGCTATCTGATGCTGCTGCTGCTGCTGCTGCTGCT 427
371 CTCAGACTCTGAGCACTGGAATTTGCTATCTGATGCTGCTGCTGCTGCTGCTGCTGCT 430
428 TCATGCAATATGAGCGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 487
431 TCTTATGTAATGAGCGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490
488 GTGAACCTGGAATTTTAAAGTGTACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
491 GTGAACCTGGAATTTTAAAGTGTACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
548 TGAATCCCATCTTGTATGCTTATTTTGAAGCGCCATATTTTATGAGCTGTGGAAG 607
551 TGAATCCCATCTTGTATGCTTATTTTGAAGCGCCATATTTTATGAGCTGTGGAAG 610
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668 ACCAGGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
668 TCTGAGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
728 AAACAATCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787
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788 TAAAGACCTTAAAG 847
788 CAAGAACAAG 847
848 ATTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907
848 ATTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907
908 AGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967
908 AGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967
968 CAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1027
968 CAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1027
1028 CATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1087
1028 CATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1087
1088 AAGCTTTGAGAGAGCTTCTGGAATACTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1147
1088 AAGCTTTGAGAGAGCTTCTGGAATACTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1147

Db 1088 AGCGCTTCAAAAAGCTTCTTGAATAATTTTGTATTAATAAAGCAACCTTACATCAC 1147
Qy 1148 ACAACCG 1154
Db 1148 AACACAG 1154

RESULT 6
US-09-875-076-13
Sequence 13, Application US/09875076
Publication No. US20030017528A1
GENERAL INFORMATION:
Applicant: Chen, Ruoping
Applicant: Dang, Huong T.
Applicant: Liaw, Chen W.
Applicant: Lin, I-lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/141,448
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/156,553
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,633
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,555
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,634
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,294
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,293
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-09-875-076-13

Query Match 57.7%; Score 675; DB 10; Length 1173;
Best Local Similarity 74.9%; Pred. No. 5,9e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Oy	8	CAATTAACAGTACATGCGCTTAACTGAATTAATTTCTTGGACATTTTAATGCTT	67
Dp	11	CTAATAGACAAATCAATTTATATCACTAGACATCGCTTACTTTAGCAATTTTATGCTT	70
Oy	68	TACTAGCTATTGCTATAATGTTAGGCAATGTCGTGTCATTTTAGCTTTATGTGACA	127
Dp	71	TAGTAGCTTTTGGCTATTAATGCTAGGAATGCTTGGTCATTTTAGCTTTTGGGGAC	130
Oy	128	GAAATCTTAAACATCGAAGTAATTACTTTTCTTAACCTTGGCCATTCGACATCTCTTG	187
Dp	131	AAACCTTAGACATCGAAGTAGTAATTTTCTTAACTGTGGCCATCTGTACATTCCTT	190
Oy	188	TGGGTGCAATTTGCAATTTCTCTGTACATACCTTCTCGCTGACTTACGACCTTCTGAA	247
Dp	191	TGGGTGTATCTCCATCTCTTTGTATGATCCCTGCACAGCCTGTGTGAAATTTTGAA	250
Oy	248	AGCAAGCTTGTGTATTTTGGCTCATTTACTGACTATCTTTATGTACAGCATCTGTAT	307
Dp	251	AGGAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACACATCTGTATTA	310
Oy	308	ATATTGCTCATGACTACGATGCGTACGATGCGTACAAATGCGGTGTATTAAG	367
Dp	311	ACATTGCTCATGACTACGATGCGTACATCTGTACATCTGAAATGCTGTCTTATTA	370
Oy	368	CTACGACTTTGGCACTGGAATAATTTGCTACTGACATGATGTGGCTGTTTGATCTTCT	427
Dp	371	CTCAACATACTGGGGTCTTTGAAGAATGTTTATCTGTATGATGGCGGTTTGGGGTGGCT	430
Oy	428	TCATGACAAATGGGCGCATGATCTGATTTCAAGATCTTTGGCAGAAATGACTACAGAT	487
Dp	431	TCTTAGTAATGGGCGCAATGATTTAGTTCATGATCTTTGAAGGATTAAGGTAGTAT	490
Oy	488	GTGAACCTGATTTTAAAGATGATCTTGTGCTCTCCCTACATCATTTATGGAATCC	547
Dp	491	GTGAACCTGGAATTTTTCGGAAATGATCATCTTGGCATACATCATTTCTTGGAAATCG	550
Oy	548	TGATTCCTCATCTTGTAGTTGCTTATTTTCAAGCGCCCATATTTACTGAGCCTGTGGAAGC	607
Dp	551	TGATTCCTCATCTTGTAGTTGCTTATTTTCAATGAATATTTATTTGAGCCTGTGGAAGC	610
Oy	608	GAGAGAACTGAGAGGTGCTCAGACCAACCTGTACTCCCTGTGACTCTTTCAGCACTG	667
Dp	611	GTGATCATCTCAGTAGGTGTCCAAGCCATCTGTGACTGATGCTGTCTCTTCCACA---	667
Oy	668	ACCAAGCACTCTCTGAGACAGACCCCGATTCAGAGGCGCATCTGCGCAGACGGAAG	727
Dp	668	TCTGTGACACATCATTTAGAGGTAGTACTATCTTCAAGAGATCTCTTCTGTGATGACG	727
Oy	728	AAACAACCTGCTCTTGTGTTTCAAGTACCGAGAAAGCAAGTCTCTTGTGTTTCCA	787
Dp	728	AAATTCCTGTACATCTTATTTCAATTCAGAGAACAGAGGAAGAAAGTAGTCTCAGTGTCTT	787
Oy	788	TAAAGACCTACAAAGACAGCAATGTGATGCTTCCAAATGGGCTCTCTCCACTCAG	847
Dp	788	CAGAAGCAAGATGAATAGCAATACATTTGCTTCCAAATGGGTTCTCTTCCCAATCAG	847
Oy	848	ATTCTCTGTGCTTTAGCAAAAGGGAACATATGAACTTTTCAAGCCAGGAATTAGCCA	907
Dp	848	ATTCTGTATGCTTTTCCAAAGGGAACATGTTGAATCTCTTAGAGCCAGAGATTAGCCA	907
Oy	908	AGTCACTGAGCAATCTTTAGCAGCTTTTGGCATTTGTGCGGGCTGCATATTTACATGACT	967
Dp	908	AGTCACTGAGCAATCTTTAGGAGGTTTGTGCTGTTTGTGCGGGCTGCATATTTCTCTGTCCA	967
Oy	968	CAGTTATCTACTCATTTTTTCTGAAAGGAATTGACTAAATCAACCTGTATCCATACTG	1027
Dp	968	CAATGTCTCTTATTTATTTCTCAGCAACAGTCTTAATCAGTTTGTATATAGAAATTG	1027
Oy	1028	CCTTTTGGCTCAGAGGTTCAAATCTCTTGTTAATCCCTTTTGTATCATTGTGTACA	1087
Dp	1028	CATTTTGGCTCAGAGGTTCAAATCTCTTGTCAATCTCTTTGTATCATTGTGTACA	1087

Oy		1088 AACGTTTCAGAGCGCTTCCGAAATACACTCCTGTGAAGAGCATCACGCACAC	1147
Db		1088 AGCGTTTCAAAAGCGCTTCTTGAAATAATTGTTGTAATAAAAAAGCAACCTCTACATCAC	1147
Oy		1148 ACAACCG 1154	
Db		1148 AACACAG 1154	


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RESULT 7
US-09-876-252-13
; Sequence 13, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Brunnema, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W
; TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: ARKN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634

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PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,294
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/156,633
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-09-876-252-13

Query Match 57.7%; Score 675; DB 10; Length 1173;
Best Local Similarity 74.9%; Pred. No. 5.9e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATAACGATACGACCTTAACATCAATTAATTTCTTGACATTTTATGCTT 67
DB 11 CTAATAGCAACAATTTATCACTAGCACTGCTGTTACTTTAGCAATTTTATGCTT 70
QY 68 TACTAGCTATGCTATATAGTTAGGCAATGCGTGCATTTTATGTTAGTGGACA 127
DB 71 TAGTACTTTTGTATATAGCTAGGAAATGCTTGGCATTTTATGCTTGTGGACA 130
QY 128 GAAATTTAGACATCGAAGTAATTAATTTTCTTAACTTGGCATTTGACATTTCTT 187
DB 131 AAAACCTTAGACATCGAAGTAATTTTCTTAACTTGGCATTTGACATTTCTT 190
QY 188 TGGGTCATTTGCAATTCCTCTGTACATTCCTCGGAGACTTGTGACATTTGAGAA 247
DB 191 TGGGTGATCTTCATCTCTTCTTGTACATTCCTCGGAGACTTGTGAGAA 250
QY 248 AGCAACCTTGTATTTTGGCTCATTAAGTACTATCTTTATGATAGCAATCTGTATTA 307
DB 251 AGGAATCTGTATTTTGGCTCATTAAGTACTATCTTTATGATAGCAATCTGTATTA 310
QY 308 AATTTGCTCATGCTAGATGCTGCTACGATGCTGCAATGCCGTGTGATAGAG 367
DB 311 ACATTTGCTCATGCTAGATGCTGCTACGATGCTGCAATGCCGTGTGATAGAA 370
QY 368 CTCAGACCTGCGACCTGGAAATGCTACGATGCTGCTGCTGCTGCTGCTGCT 427
DB 371 CTCAGACCTGCGACCTGGAAATGCTACGATGCTGCTGCTGCTGCTGCTGCT 430
QY 428 TCATGCAAAATGGCGGATGATCTGATTTCAAGCTTTGGCAGAAATAGCACTACAGAA 487
DB 431 TCTTATGATAGTGGCCAAATGATTTCTAGTTCAAGCTTTGGCAGAAATAGTGAAT 490
QY 488 GTGACCTGGATTTTAAAAAGTGTACTTGTCTCTCCCTACATCAATTTGAATTC 547
DB 491 GTGACCTGGATTTTAAAAAGTGTACTTGTCTCTCCCTACATCAATTTGAATTC 550
QY 548 TGAATCCCAATCTGTTAGTGTCTTATTTAGCGCCCATATTTAGAGCTGTGAGAG 607
DB 551 TGAATCCCAATCTGTTAGTGTCTTATTTCAACATGAATATTTAGAGCTGTGAGAG 610
QY 608 GAGAGAAATGACAGGTGCTGAGCACTGTAATCTCCCTGTAATCTTCCAGCAGT 667
DB 611 GTGATCATCTCAATAGTGTGCAAGCATCTGGAATGCTGTCTTCCAGCA--- 667
QY 668 ACCAGGACATCTCTGAGACAGAGCCGATTCAGAGGCGCATCTGCGACAGCAGAA 727
DB 668 TCTGTGACACATCTATCAGAGTATGACTATCTTCAAGAGATCTCTTTCTGACATCAG 727

QY 728 AAACAATGCTCTCTTGGTTCAGACAGTCAAGGAGAAAGACAGTCTCTGTTTCCA 787
DB 728 AATCTCTGATCTCTTCAATTCAGAGAGCAGAGGAGAAAGATGATCTATGTTTCT 787
QY 788 TAAAGCTTACAAAGACAGCATGATGCTTCCAAATGGCTTCTCTCCACTCAG 847
DB 788 CAAGAACCAAGATGAAATAGCAATATGCTTCCAAATGGCTTCTCTCCAAATCAG 847
QY 848 ATTCCTGCTCTTCCAGAAAGGAAATATGAACTTTTCAAGCAGGAAATTTAGCCA 907
DB 848 ATTCCTGCTCTTCCAGAAAGGAAATATGAACTTTTCAAGCAGGAAATTTAGCCA 907
QY 908 AGTCACTGGCCATCTTATAGCAGTCTTGGCATTTGCTGGCTCATATTTCACTGATA 967
DB 908 AGTCACTGGCCATCTTATAGGCTTTTGTGCTTTGCTGGCTCATATTTCTGTTCA 967
QY 968 CAGTTATCTATCTATTTTCTGAAAGAACTTGAATCAACCTGTGACATATCTG 1027
DB 968 CAGTTATCTATCTATTTTCTGAAAGAACTTGAATCAACCTGTGACATATCTG 1027
QY 1028 CTTTGGCTCCAGGCTTCAATTCCTGTTATCCCTTTTGTATCCATGTTGTCACA 1087
DB 1028 CATTGGCTTCAAGTGTTCATTCCTGTTATCCCTTTTGTATCCATGTTGTCACA 1087
QY 1088 AACGTTTCAAGAGCTTCTCTGAAATATCTTCTGTGAGAGCAATCCAGCCACAC 1147
DB 1088 AGGCTTTCAAGAGCTTCTCTGAAATATCTTCTGTGAGAGCAATCCATCAGAC 1147
QY 1148 ACAACCG 1154
DB 1148 AACACAG 1154

RESULT 8
US-10-052-193-1
Sequence 1, Application US/10052193
Publication No. US20020132755A1
GENERAL INFORMATION:
APPLICANT: Pfizer, Inc.
TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
FILE REFERENCE: PCT/0963A
CURRENT APPLICATION NUMBER: US/10/052,193
CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 0101223.6
PRIOR FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-10-052-193-1

Query Match 57.7%; Score 675; DB 13; Length 1173;
Best Local Similarity 74.9%; Pred. No. 5.9e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATAACGATACGACCTTAACATCAATTAATTTCTTGACATTTTATGCTT 67
DB 11 CTAATAGCAACAATTTATCACTAGCACTGCTGTTACTTTAGCAATTTTATGCTT 70
QY 68 TACTAGCTATGCTATATAGTTAGGCAATGCGTGCATTTTATGTTAGTGGACA 127
DB 71 TAGTACTTTTGTATATAGCTAGGAAATGCTTGGCATTTTATGCTTGTGGACA 130
QY 128 GAAATTTAGACATCGAAGTAATTAATTTTCTTAACTTGGCATTTGACATTTCTT 187
DB 131 AAAACCTTAGACATCGAAGTAATTTTCTTAACTTGGCATTTGACATTTCTT 190
QY 188 TGGGTCATTTGCAATTCCTCTGTATACATCTTCTGCTGACTTACTGACATTTGGA 247
DB 191 TGGGTGATCTTCATCTCTTGTATACATCTTCTGACAGCTGCTGCTGATGGAATTTGGA 250

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248 AGCAAGCTGTGTATTTGGCTCATCTACTATCTTTATATGACAGATCTGTATATA 307
251 AGGAATCTGTGTATTTGGCTCATCTACTATCTTTATATGACAGATCTGTATATA 310
308 ATATTGTCTCTATCAGTACGATCGCTACAGTCTCAAAATGCCGTGTGTATAG 367
311 ACATTGTCTCTATCAGTACGATCGCTACAGTCTCAAAATGCCGTGTGTATAG 370
368 CTCAGCACTGTGGCAGCTGGAATAATGCTACTCAGATGGTGGCTGTGGATATCTCT 427
371 CTCACATATCTGGGCTTTGAAGATTTGTTACTCTGATGGTGGCTGTGGATATCTCT 430
428 TCATGACAAATGGCCGATGATTTCTGATTTGAGCTTTGGCAGAAATAGCAATACAGAT 487
431 TCTTAGTAATGGCCCAATGATTTCTAGTTTCAGAGCTTTGGAAGATGAAGTAGAT 490
488 GTGAACCTGTGATTTTAAAGAGTGTACTTGTCTCTCCCTCATCATCTATTTAGAAATTC 547
491 GTGAACCTGTGATTTTTCGGAATGTGTATCTCTTGCATCATCATCTATTTGGAATTCG 550
548 TGATCCCATCTTGTAGTGTCTTATTTTCAGGGCCCATTTACTGAGCCTGTGGAAGC 607
551 TGATCCCATCTTGTAGTGTCTTATTTTCAGGGCCCATTTACTGAGCCTGTGGAAGC 610
608 GAGAGAACTGAGCAGGTGCTCAGCCACCTGTACTCTCCCTCTGACTCTTTCAGCAGTG 667
611 GTGATCATCTCAGTAGTGCTCAAGCCATCTGAGCTGCTGCTCTCTTCCACA--- 667
668 ACCAGGACATCTCTGAGCAGACAGACCCCATTTCAAGGGCCCTGTGCAAGCAGGAAG 727
668 TCTGTGACATCTCAGTAGTGCTCAAGCCATCTGAGCTGCTGCTCTTCTGTGATGACAG 727
728 AAACAACCTGCTCTGTGGTTGAGCAAGTCAAGCAGGAAGAGCAGTCTTGTGTTTCCA 787
728 AAGTTCCTGAGTCTTCTTATTCAGAGAGCAGAGAGAGAGAGTCTGCTGCTGTTTCT 787
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1028 CTTTGTGCTCAGGCTTCAATCTCTGTTAATCCCTTTTGTATGATGATGATGATGATGAT 1087
1028 CTTTGTGCTCAGGCTTCAATCTCTGTTAATCCCTTTTGTATGATGATGATGATGATGAT 1087
1088 AACGTTTTCAGAAAGCTTCTGAAATATCTCTGTGAGAGAGCAAGCAGCAGCAGC 1147
1088 AACGTTTTCAGAAAGCTTCTGAAATATCTCTGTGAGAGAGCAAGCAGCAGCAGCAGC 1147
1148 AACACCG 1154
1148 AACACCG 1154

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RESULT 9

US-10-272-983-13
 ; Sequence 13, Application US/10272983
 ; Publication No. US20030148450A1

GENERAL INFORMATION:

APPLICANT: Chen, Ruoping
 APPLICANT: Dang, Huong T.
 APPLICANT: Liaw, Chen W.

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APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/10/272,983
PRIOR FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 13
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-10-272-983-13

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Query Match 57.7%; Score 675; DB 15; Length 1173;
 Best Local Similarity 74.9%; Pred. No. 5,9e-185;
 Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

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8 CAATTAACAGTACATCCCTTAAATCAATTAATTAATTTTGAATTTTAAATGCTT 67
11 CTAATAGCAATCAATTTATATCACTAGACATCGTGTACTTTAGCATTTTATGCTCT 70
68 TACTAGCTATTTGCTTAAATGTTAGGCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
71 TAGTAGCTTTTGTCTAATAGCTAGGAATGCTTGTGCTATTTAGCTTTTGTGAGACA 130
128 GAAATCTTACAGTACATTTCTTTTCTTAACTTGGCCATGAGACTTCTTGT 187
131 AAAACCTTACAGTACATTTCTTTTCTTAACTTGGCCATGAGACTTCTTGT 190
188 TGGGTGCAATGCAATTCCTCTGTACATACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 247
191 TGGGTGCAATGCAATTCCTCTGTACATACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 250
248 AGCAAGCTGTGTATTTGGCTCATCTACTGATCTTCTTTATATGACAGATCTGTGTATA 307
251 AGGAATCTGTGTATTTGGCTCATCTACTGATCTTCTTTATATGACAGATCTGTGTATA 310
308 ATATTGTCTCTATCAGTACGATCGCTACAGTCTCAAAATGCCGTGTGTATAG 367
311 ACATTGTCTCTATCAGTACGATCGCTACAGTCTCAAAATGCCGTGTGTATAG 370
368 CTCAGCACTGTGGCAGCTGGAATAATGCTACTCAGATGGTGGCTGTGGATATCTCTCT 427
371 CTCACATATCTGGGCTTTGAAGATTTGTTACTCTGATGGTGGCTGTGGATATCTCTCT 430
428 TCATGACAAATGGCCGATGATTTCTGATTTGAGCTTTGGCAGAAATAGCAATACAGAT 487
431 TCTTAGTAATGGCCCAATGATTTCTAGTTTCAGAGCTTTGGAAGATGAAGTAGAT 490
488 GTGAACCTGTGATTTTAAAGAGTGTACTTGTCTCTCCCTCATCATCTATTTAGAAATTC 547
491 GTGAACCTGTGATTTTTCGGAATGTGTATCTCTTGCATCATCATCTATTTGGAATTCG 550

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QY	548	TGATCCCATCTTGTAGTACTTATTTACAGGCGCCAAATTATCTAGGAGCGCTGGGAAGC	607
Db	551	TGATCCCATCTTGTAGTACTTATTTACAGGCGCCAAATTATTTATTTAGGAGCGCTGGGAAGC	610
QY	608	GAGAGAACTGAGGAGGTGCTCAAGCCACCCTGTATCTCCCTGTACTCTTCCAGCAAGTG	667
Db	611	GTGATCATCTCAGTAGGTGGCCAAAGGCCATCTGTGAGCTGACGTGTGTCTTCCAAACA---	667
QY	668	ACACGCAATCTCTGACAGACAGAACCCCAATTCAAGGCGCATCTGCGACAGAGAAAG	727
Db	668	TCTGTGACACTCTATTCAGAGTAGACTATCTTCAAGAGATCTCTTCTGCATGACAG	727
QY	728	AAACAACGCTCTCTTGGTTCAGACAAAGTCAAGGAGAAAGAGAGAGTCTTGTTTTCCA	787
Db	728	AAAGTTCTGCATCTCTTTCATTCAAGAGACAGAGAGAAAGAGTAGTCTCATGTTTTCTT	787
QY	788	TAAAGGCTTACAAAGAACAGCAATGTGATCGCTTCCAAAATGAGGCTTCTCTCCACTCAG	847
Db	788	CAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGAGGTTCTTCCCAATCAG	847
QY	848	ATTCCCTGCGCTTCTCAGAAAGGGAACATATCGAACTTTTCAAGAGCCAGAAATTAGCA	907
Db	848	ATTCTGTAGCTCTTTCACCAAGGGGAACATGTGAACTGTCTTAGAGCCAGAGAAATTAGCA	907
QY	908	AGTCACTGGCCATTAATCTTTAGCAGCTTTGTCATTTGCTGGGCTTCCAAATTCATCTGACTA	967
Db	908	AGTCACTGGCCATTAATCTTTAGGAGGTTTTTGTCTTTGCTGGGCTTCCAAATTCATCTGACTA	967
QY	968	CAGTTATCTACTATTTTTCCTGAAAGAACTTGACTTAAATCAACTGTATACATATCTG	1027
Db	968	CAATTTGCTCTTCAATTTATTCCTCAGCAACAGGCTTAAATCAGTTGGTATGAATTTG	1027
QY	1028	CCTTTTGGCTCCATGTGTTCAATTCCTTGTAAATCCCTTTTGTATTCATTTGTGTACA	1087
Db	1028	CATTTTGGCTTCAGTGTTCATTTCTTTGTCAATTCCTTTTGTATTCATTTGTGTACA	1087
QY	1088	AACGTTTTCAGAAAGGCTTTCCTGAAAATACTTCTGTGAGAAAGCAATCCAGCCACCA	1147
Db	1088	AGCCCTTTCAAAAGGCTTTCCTTGAAAATATTTTGTATTAATAAAGCAACTTACCATCAC	1147
QY	1148	ACAACCG	1154
Db	1148	AACACAG	1154
RESULT 10			
US-10-354-769-1			
Sequence 1, Application US/10354769			
Publication No. US20030149242A1			
GENERAL INFORMATION:			
APPLICANT: Pfizer Inc.			
APPLICANT: O'Reilly, Mark A.			
TITLE OF INVENTION: NOVEL POLYPEPTIDE			
FILE REFERENCE: PCI0373B			
CURRENT APPLICATION NUMBER: US/10/354,769			
CURRENT FILING DATE: 2003-01-30			
PRIOR APPLICATION NUMBER: US 09/698,801			
PRIOR FILING DATE: 2000-10-27			
PRIOR APPLICATION NUMBER: US 60/211,243			
PRIOR FILING DATE: 2000-06-14			
PRIOR APPLICATION NUMBER: GB 9925641.4			
PRIOR FILING DATE: 1999-10-29			
PRIOR APPLICATION NUMBER: GB 0009973.9			
PRIOR FILING DATE: 2000-04-20			
NUMBER OF SEQ ID NOS: 10			
SOFTWARE: Patentin version 3.1			
SEQ ID NO 1			
LENGTH: 1173			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-10-354-769-1			

Qy	1028	CGTTTGGCTCAGGTTCAATCCTTGTAAACCTTTTGTATCCATTGTGAC	1087
Db	1028	CATTTTGGCTCAGGTTCAATCCTTGTCAACCTTTTGTATCCATTGTGTCA	1087
Qy	1088	AACGTTTCAGAAAGCTTCCGAAAAATACCTCGTAGAAGGCAATCCAGCCACC	1147
Db	1088	AGCGCTTTCAAAAGGCTTCTTGAAAAATATTTGTATAAAAAAGCACTTCACCATAC	1147
Qy	1148	ACAAACCG	1154
Db	1148	AACACAG	1154

RESULT 11

US-10-393-807-13
; Sequence 13, Application US/10393807
; Publication No. US20030175891A1
JOURNAL INFORMATION

Query Match	57.7%	Score 675:	DB 16:	Length 1173:
Best Local Similarity	74.9%	Pred. No. 5.9e-185:		
Matches 859, Conservative	0:	Mismatches 285:	Indels 3:	Gaps 1:

Db	191	TGGGTGATGATCTCCATTCCTTTTGATCAATCCCTCACAGAGCTGTTGGAAATTTTGGAA	250
Oy	248	AGCAAGCTTGATATTTTGGCTCATTAAGTACTATCTTTATGTACAGCATCTGTGTATA	307
Db	251	AGGAAATCTGTGATATTTTGGCTCACTACTGACTATCTGTATGTACAGCATCTGTATATA	310
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Db	311	ACATTGTCCATAGCTATGATGATGATACCTGTGAGTCCAAATGTCTGTGCTTATAGAA	370
Oy	368	CTCAGCACTCTGGCACCCTGGAAAAATTTGCTACTCAGATGATGTGGCTGTTTGGATATTCTCT	427
Db	371	CTCAACATACCTGGGGCTTTGAAATTTGTACTGTGATGATGGCCGCTTTTGGGTGCTGCT	430
Oy	428	TCATGACAAATGGGCGCATGATTTGTGATTTTCAGACTCTTGGCAGAAATGACTACAGAAAT	487
Db	431	TCTTAGTAATATGGGCGCAATGATTTCTAGTTTTCAGAGTCTTGGAAAGATGAAGTGTAAAT	490
Oy	488	GTAAGCCGTGATTTTTTAAAAAGGAGTACCTTGTGCTCCGTAACATCATTTATGGAAATTC	547
Db	491	GTAAGCCGTGATTTTTTTTGGAAATGTACATCTTGCATCAATCATATTTCTTGGAAATTC	550
Oy	548	TGATCCCATCTTGTGTATGTGCTTATTTTCAGCGCCCATTTTACTGGAGCTGTGGAAAG	607
Db	551	TGATCCCATGATCTTATGTGCTTATTTTCAACATGAATATTTATTTGAGCGCTGTGGAAAG	610
Oy	608	GAGAGAAATGAGCAGGTGCTTACAGCCACCTGTATCTCCCTGTGACTCTTTCCAGCAGTG	667
Db	611	GATGATCATCTCAGTAGGTGGCCAAAGCCATCTGTGACTGATGCTGTCTTCCAAACA---	667
Oy	668	ACCAAGGACACTCCTGAGACAGGACCCCGATTTCAAGGGGGACTCTGCACAGCAGGAAG	727
Db	668	TCTGTGACACTCATTTAGAGGTAGTACTATCTTTAAGAGATCTCTTTTCTGCATCGACAG	727
Oy	728	AAACAATGCTCTCTTGTGTTCAGACAAAGTACAGCGAAAAAGCAGTCTCTGTTTTTCA	787
Db	728	AAATTCCTGATCTTTTCATTTAGAGAGACAGAGGAAGAAAGATGATCTATGTTTTCT	787
Oy	788	TAAAGCTTACAGAAACAGCAATGTATCGCTTCCAAATATGGGCTTCTCTCCACTCAG	847
Db	788	CMAAACAACCAAGATTAATAGCAATTAATTTCTTCCAAATATGGGTTCTTCTCCCAATCAG	847
Oy	848	ATTCCCTGTGCTCTTACAGAAAGGGAATATATCGAACTTTTCAGAGCCAGGAAATTTAGCA	907
Db	848	ATTCTGTAGCTCTTACCAAAAGGGAATGTGAACTGTAGCTTTAGCCAGAGATTTAGCA	907
Oy	908	AGTCACTGGCCATTAATCTGTAAGGGATTTTGTGCTGTTTCTGGGCTCCAAATATCTCTGTTCA	967
Db	908	AGTCACTGGCCATTAATCTGTAAGGGATTTTGTGCTGTTTCTGGGCTCCAAATATCTCTGTTCA	967
Oy	968	CAGTTATCTACTATTTTTTCTGAAAGGAATTTGATTAATCAACTGTGATCACTACTG	1027
Db	968	CAATTTGCTCTTCAATTTATTTCTCAGCAACAAGGCTCTTAATCATGTTTGGATATGAATTTG	1027
Oy	1028	CCTTTGGGCTCAGTGGTCAATCTTTTGTATATCCCTTTTGTATCTCATTTGATGTACCA	1087
Db	1028	CATTTTGGCTCAGTGGTCAATTTCTTTGTCAATCTCTTTTGTATCTCATTTGATGTACCA	1087
Oy	1088	AACGTTTTCAAGAGCTTCTCTGAAAAATCTCTCTGTGAGAGGCAATCCACGCAACAC	1147
Db	1088	AGCGCTTTCAAAAGGCTTCTTGAAATATTTTGTATAAAAAAGCAACTCTACATCATAC	1147
Oy	1148	ACAACCG 1154	
Db	1148	AACACAG 1154	

QY	128	GAATCTACACATCGAGTAATTACTTTTCTTAACTTGGCCATTGAGACTTCTT	187	RESULT 12
			US-10-417-820A-13	
Db	131	AAAACCTTAACATCGAAGTAGTATTATTTTCTTAACTTGGCCACTTCTTGACTTCTT	190	; Sequence 12A, Application US/10417820R
			; Publication No. US20030229216A1	
QY	188	TGGGTGCAATTGCAATTCCTCTGACATACCTCCCTCGGTGACTTACAGCATTTCTGAA	247	; GENERAL INFORMATION:
				; APPLICANT: Chen, Ruoping

APPLICANT: Liaw, Chen W.
APPLICANT: Lowitz, Kevin
APPLICANT: Chalmers, Derek T.
APPLICANT: Behan, Dominic P.
TITLE OF INVENTION: Conceptually Activated Human G Protein Coupled
FILE REFERENCE: 7.US28.CON
CURRENT APPLICATION NUMBER: US/10/417,820A
CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,951
REMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn version 3.2
SEQ ID NO 13
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-10-417-820A-13

Query Match 57.7%; Score 675; DB 17; Length 1173;
Best Local Similarity 74.9%; Pred. No. 5.9e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATACAGTACATCGCTTAACATCAATTAATTTCTTGACATTTTATGCTT 67
DB 11 CTAATGACACATCAATTTATCTACAGACCTGCTTACTTTAGCATTTTATGCTT 70
QY 68 TACTAGCTTATGCTTAATGTTAGGCAATGCTGCTGCTTATGCTTTATTTAGTGA 127
DB 71 TAGTACTTTTGTATATATGCTAGGAATGCTTGGTCATTTTATGCTTTGTGTGACA 130
QY 128 GAAATTTAGACATCGAATTAATTTCTTTTCTTAATCTGGCATTTGACATTTCTTTG 187
DB 131 AAAACCTTGACATCGAATGATTTATTTTCTTAACTTGGCATCTTGAATTTCTTTG 190
QY 188 TGGGTGCAATTTGCTCTGCTGATACATCTTCTGCTGCTGCTTACTTTGACCTTTGAA 247
DB 191 TGGGTGCTATCTCATTTCTTTGATACCTCTCACAGCTGCTTGCATGATGATTTGAA 250
QY 248 AGCAAGCTTGTATTTTGGCTCATTAAGTACTATCTTTTATGATGACATCTGTATTA 307
DB 251 AGGAATCTGTATTTTGGCTCATTAAGTACTATCTTTTATGATGACATCTGTATTA 310
QY 308 ATATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 367
DB 311 ACATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 370
QY 368 CTCAGACTTGGCAGCTGGAATTTGCTACTCAGATGCTGCTGCTTGTATTTCTCT 427
DB 371 CTCAGACTTGGCAGCTTGTGAATTTGCTACTCAGATGCTGCTGCTTGTATTTCTCT 430
QY 428 TCATGCAAAATGGGCGGATGATTTCTGATTTTCAAGCTTCTGGCAATAGACATGCAAT 487
DB 431 TCCTAGTGAATGGGCGGATGATTTCTGATTTTCAAGCTTCTGGCAATAGATGCAAT 490

QY 488 GTGACCTGATTTTAAAAAGGATGATTTGCTCTCCCTACATCATTTAGGAATTC 547
DB 491 GTGACCTGATTTTAAAAAGGATGATTTGCTCTCCCTACATCATTTAGGAATTC 550
QY 548 TGATCCCATCTTGTATGTTCTTATTTTCAAGCCCATATTTTACGTGAGCTGTGAAGC 607
DB 551 TGATCCCATCTTGTATGTTCTTATTTTCAAGCCCATATTTTACGTGAGCTGTGAAGC 610
QY 608 GAGGAAATCTGACAGGTGCTTACGCCCTGTACTTCCCTGTGATCTTTCCAGCATG 667
DB 611 GTATCATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
QY 668 ACCAGGACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 727
DB 668 TCTGTGACATCTATTCAGAGTATGATGATGATGATGATGATGATGATGATGATGAT 727
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DB 728 AAATCTGATCTTCTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 787
QY 788 TAAGGCTTATCAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 847
DB 788 CAAGAACTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 847
QY 848 ATTCCGCTGCTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 907
DB 848 ATTCTGATCTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 907
QY 908 AGTCACTGCTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 967
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QY 1028 CTTTGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1087
DB 1028 CTTTGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1087
QY 1088 AACGTTTCAAGAAAGGCTTCTGAAATATCTTCTGTAAGCAATGATGATGATGATGAT 1147
DB 1148 AACGTTTCAAGAAAGGCTTCTGAAATATCTTCTGTAAGCAATGATGATGATGATGAT 1147
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DB 1148 AACGTTTCAAGAAAGGCTTCTGAAATATCTTCTGTAAGCAATGATGATGATGATGAT 1147

RESULT 13
US-10-349-253A-1
Sequence 1, Application US/10349253A
Publication No. US2004004339A1
GENERAL INFORMATION:
APPLICANT: Aubart, Kelly
APPLICANT: Bergema, Derek
APPLICANT: Fitzgerald, Laura
APPLICANT: Graybill, Todd
APPLICANT: Li, Xiaolong
APPLICANT: Michalovich, David
APPLICANT: Morrow, Dwight
APPLICANT: Zhu, Yuan
TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
FILE REFERENCE: GP70655-2C2
CURRENT APPLICATION NUMBER: US/10/349,253A
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 09/910,411
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 09/693,761
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/431,898
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapien
US-10-349-253A-1

Query Match 57.7%; Score 675; DB 18; Length 1173;
Best Local Similarity 74.9%; Pred. No. 5,9e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

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QY 8 CAATAACAGTACATCGCCTTAACATCAATTAATTTCTTGAATTTTAAATGCT 67
DB 11 CTAATAGCAGATCAATTTATCACTAGACCTCGTTACTTTAGCATTTTATGCT 70
QY 68 TACTAGCTATTGCTAATATGTTAGGCAATGCTGCTATTTTAACTTTTATTTGAGCA 127
DB 71 TAGTAGCTTTTCTAATAGTAGAGAAATGCTTGGTCTTTAGCTTTTGTGTGAGCA 130
QY 128 GAAATCTTAGAGATGAATATTAATTTTCTTAACTTTGAGCAATGAGCTTTTG 187
DB 131 AAAACCTTAGACATGAATGATTTATTTTCTTAACTTTGAGCAATGAGCTTTTG 190
QY 188 TGGGTGCAATTCCTCTGTCATACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 247
DB 191 TGGGTGATCTTCATCTCTTTTGTACATCTCTGCTGCTGCTGCTGCTGCTGCTG 250
QY 248 AGCAAGCTTGTATTTTGGCTCATATTAATGCTGCTGCTGCTGCTGCTGCTGCTG 307
DB 251 AGGAATCTGTATTTTGGCTCATATTAATGCTGCTGCTGCTGCTGCTGCTGCTG 310
QY 308 ATATGCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 367
DB 311 AATTTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 370
QY 368 CTGACGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 427
DB 371 CTGACGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 430
QY 428 TCATGACAAATGGCCGATGATTTGATTTGATTTGATTTGATTTGATTTGATTT 487
DB 431 TCTTGTGATGGCCGATGATTTGATTTGATTTGATTTGATTTGATTTGATTT 490
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DB 491 GTGAACCTGATTTTAAAGTGTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 550
QY 548 TGATCCCATCTTGTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
DB 551 TGATCCCATCTTGTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610
QY 608 GAGAGAACTGAGAGGCTGCTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667
DB 611 GTGATCATCTGAGAGGCTGCTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 667
QY 668 ACCAGGACACTGCTGAGAGGCTGCTGAGCCCTGCTGCTGCTGCTGCTGCTGCT 727
DB 668 TCTGTGAGACACTGCTGAGAGGCTGCTGAGCCCTGCTGCTGCTGCTGCTGCTG 727
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DB 728 AAGTTCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787
QY 788 TAAGAGCTTACAGAGGCTGCTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 847
DB 788 CAAGAGCTTACAGAGGCTGCTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 847
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DB 848 ATTCTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907
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QY 908 AGTACGCGCATATCTTACAGCTTTTGGCATTTGCTGCGCTCCATATTCATGACTA 967
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QY 968 CAGTTATCTACTATTTTCTCTGTAAGAGAACTGATTAATCAACCTGATGCACTG 1027
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QY 1028 CTTTGGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1087
DB 1028 CATTGTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1087
QY 1088 AACGTTTTCAGAGGCTTCTGTAAGAAATACCTTCTGTAAGAGGCAATCCAGCCAC 1147
DB 1088 AGCGCTTTCAGAGGCTTCTGTAAGAAATACCTTCTGTAAGAGGCAATCCAGCCAC 1147
QY 1148 ACAACCG 1154
DB 1148 AACACAG 1154
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RESULT 14
US-10-723-955-13
Sequence 13, Application US/10723955
Publication No. US20040110238A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lin, I-Lin
APPLICANT: Liaw, Chen W.
APPLICANT: Lehman-Bruhlma, Karin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Gore, Martin
APPLICANT: White, Carol
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: 7 US29, CON
CURRENT APPLICATION NUMBER: US/10/723, 955
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 10/417, 820
PRIOR FILING DATE: 2003-4-16
PRIOR APPLICATION NUMBER: 09/416, 760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170, 496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110, 060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120, 416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121, 852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109, 213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123, 944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123, 945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123, 948
PRIOR FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.2
SEQ ID NO 13
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-955-13
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Query Match 57.7%; Score 675; DB 19; Length 1173;
Best Local Similarity 74.9%; Pred. No. 5,9e-185;

Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATACAGTACATCGCCTTAACATCAATTAATTTCTTGACATTTTATGCTT 67
DB 11 CTATAGCAACAATTAATTAACATGACCTGCTGTATCTTATGACATTTTATGCTT 70
QY 68 TACTAGCTATTTGCTATTAATGTTAGGCAATGTCGTCATTTTATGCTTATGAGCA 127
DB 71 TGTAGCTTTTGTATTAATGCTAGGAAATGCTTGTGCTTTTATGCTTTGTGTGACA 130
QY 128 GAAATCTTGAACATCGAAGTAATTAATTTTCTTAACTTGGCCATTTGACATCTTTG 187
DB 131 AAAACCTTGAACATCGAAGTAATTTTCTTAACTTGGCCATCTGACTCTTTG 190
QY 188 TGGGTCATTTGCAATTTCTCTGATACATCTTCTGCGGACTTCTGACTTCTGGA 247
DB 191 TGGGTCATTTGCAATTTCTCTGATACATCTTCTGCGGACTTCTGACTTCTGGA 250
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QY 308 AATTTGCTCATACGATACGATCGCTACAGTCAGTCTCAAAATGCCGTGTATAGAG 367
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QY 368 CTCAGACTCTGCGACCTGGAAAATGCTACTGATGCTGTGCTTTGATATCTCTT 427
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QY 428 TCATGCAAAATGGGCGATGATCTGATTTCAAGCTTTGGCAATATGACATACAGAA 487
DB 431 TCTTATGATAGTGGCCATATCTTATGATTTCAAGCTTTGGCAATATGACATACAGAA 490
QY 488 GTGACCTGGATTTTAAAAAGTGTACTTCTCTCTTACATCATTAATGGAATTC 547
DB 491 GTGACCTGGATTTTAAAAAGTGTACTTCTCTCTTACATCATTAATGGAATTC 550
QY 548 TGTATCCCATCTTGTATGCTTATTTTCAAGGCGCATTTTACTGAGGCTGTGAAGC 607
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QY 608 GAGAGAAATGAGCAGGTCGCTCAGCAACCTGTACTCCCTCTGACTTTCCAGAGAGT 667
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QY 668 ACCAGGACACTCTCTGACAGACAGACCCGATTCAGAGGCGACTCTGACAGACGAAAG 727
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DB 728 AAGTCTCTGATCTTTTCAATTCAGAGAGACAGAGGAGAAAGATGATCTATTTTCTT 787
QY 788 TAAGACCTTCAAGAACAGCAATGTGATCGCTTCAAAATGGGCTTCTCTCCACTCAG 847
DB 788 CAAAGAACCAAGATGAATAGCAATCAATGCTTCCAAATGGGCTTCTCTCCACTCAG 847
QY 848 AATTCCTGCTCTTCAAGCAAAAGGAAATATGCAATCTTTTCAAGACCAAGAAATAGCCA 907
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QY 908 AGTCATCTGCGCAATCTTATGAGCTTTTGGCATTTGCTGTGCTTCCATATTCAGTACTA 967
DB 908 AGTCATCTGCGCAATCTTATGAGCTTTTGGCATTTGCTGTGCTTCCATATTCAGTACTA 967
QY 968 CAGTTATCTACTATTTTCTGAAAGAACTTGAATCAATCAACCTGTATCAATCTG 1027
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QY 1028 CTTTGTGCTTCAAGTGTCAATTTCTTTGTATATCTTTTGTATCAATTTGTGACA 1087
DB 1028 CATTTTGGCTTCAAGTGTCAATTTCTTTGTATATCTTTTGTATCAATTTGTGACA 1087

QY 1088 AACGTTTCAGAGGCTTTCTTGAATAATCTTCTGTGAGAGCAATCCACCCAC 1147
DB 1088 AGCGCTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAAGCAACCTTACATCAC 1147
QY 1148 ACAACCG 1154
DB 1148 AACACAG 1154

RESULT 15
US-10-782-596-13
; Sequence 13, Application US/10782596
; Publication No. US20040137509A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Bang, Huong T.
; APPLICANT: Lin, I-Lin
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/782,596
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/875,076
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; REMAINING PRIOR APPLICATION data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-782-596-13

Query Match 57.7%; Score 675; DB 19; Length 1173;
Best Local Similarity 74.9%; Pred. No. 5,9e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATACAGTACATCGCCTTAACATCAATTAATTTCTTGACATTTTATGCTT 67
DB 11 CTATAGCAACAATTAATTAACATGACCTGCTGTATCTTATGACATTTTATGCTT 70
QY 68 TACTAGCTATTTGCTATTAATGTTAGGCAATGTCGTCATTTTATGCTTATGAGCA 127
DB 71 TGTAGCTTTTGTATTAATGCTAGGAAATGCTTGTGCTTTTATGCTTTGTGTGACA 130
QY 128 GAAATCTTGAACATCGAAGTAATTAATTTTCTTAACTTGGCCATTTGACATCTTTG 187
DB 131 AAAACCTTGAACATCGAAGTAATTTTCTTAACTTGGCCATCTGACTCTTTG 190
QY 188 TGGGTCATTTGCAATTTCTCTGATACATCTTCTGCGGACTTCTGACTTCTGGA 247
DB 191 TGGGTCATTTGCAATTTCTCTGATACATCTTCTGCGGACTTCTGACTTCTGGA 250
QY 248 AGCAAGCTTGTATTTTGGCTCATTTACTACTATCTTTTATGATAGCAATCTGTATA 307

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 16:34:25 ; Search time 3685 Seconds
(without alignments)
12085.535 Million cell updates/sec

Title: US-10-626-398-7

Sequence: 1 atcgtgcgaataacacagctac.....accgcctcaatccacttga 1170

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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8: gb_esc8:*
9: gb_esc9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	419.8	35.9	839	5	BX643713 DKFZP781C
2	410.6	35.1	704	7	CF147821 AGENCOURT
3	233	19.9	721	7	CO959034 AGENCOURT
4	127.8	10.9	853	6	CD326085 AGENCOURT
5	112	9.6	672	6	CB556920 AMGNNUC:U
6	109.2	9.3	732	7	CF147822 AGENCOURT
7	104.4	8.9	684	9	CC481311 CH240.309
8	86	7.4	643	1	AL848045 AL848045
9	83.2	7.1	499	2	BF567596 BF567596
10	76	6.5	921	9	CNS03296 CNS03296
11	75.6	6.5	663	6	BY728212 BY728212
12	75	6.4	795	6	CD804122 UI-M-GVO-
13	75	6.4	940	4	B1757352 603029570
14	75	6.4	3816	3	AK081248 M8 muscu
15	74.8	6.4	700	7	CO138455 CO138455
16	74.6	6.4	754	5	BU468854 60337878
17	74.6	6.4	716	7	CN423054 170004245
18	74.2	6.3	952	5	BX355053 BX355053
19	73.8	6.3	820	2	BP315022 601899046
20	73.4	6.3	623	7	CV026860 4931.FULL
21	73.4	6.3	812	1	AL537084 AL537084
22	73.4	6.3	887	5	BX424634 BX424634
23	73.4	6.3	902	4	B1197683 602575795
24	73.4	6.3	902	4	B1197683 602575795

25	73.4	6.3	975	1	AL536991 AL536991
26	73.4	6.3	1048	4	BM805220 AGENCOURT
27	73.4	6.3	1078	4	BM548382 AGENCOURT
28	73.4	6.3	1081	4	BM805611 AGENCOURT
29	73.4	6.3	1108	5	BM907142 AGENCOURT
30	72.6	6.2	1046	5	BQ950659 AGENCOURT
31	72.2	6.2	879	4	BI913560 AGENCOURT
32	71.8	6.1	1136	3	BC019470 Mus muscu
33	71.2	6.1	398	1	AJ661967 AJ661967
34	71.2	6.1	583	5	BP360731 BP360731
35	71.2	6.1	881	2	BF311874 BF311874
36	71.2	6.1	912	6	CB565880 AGENCOURT
37	71.2	6.1	1773	9	AY400782 Homo sapi
38	69.8	6.0	748	7	CO958889 AGENCOURT
39	69.4	5.9	889	6	CB565881 AGENCOURT
40	69.2	5.9	586	5	BP251271 BP251271
41	68.4	5.8	465	4	BI510489 BI510489
42	68	5.8	1770	9	AY400784 Mus muscu
43	68	5.8	3171	3	AK080950 Mus muscu
44	67.8	5.8	582	5	BP308119 BP308119
45	67.8	5.8	582	5	BP312753 BP312753

ALIGNMENTS

RESULT 1
BX643713
LOCUS
DEFINITION
DKFZP781C0629 r1 781 (synonym: h1cc4) Homo sapiens CDNA clone
BX643713
VERSION
BX643713
KEYWORDS
BX643713.1 GI:34478046
SOURCE
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 839)
REFERENCE
AUTHORS
Lauder, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Oanger, A.,
Fobo, G., Han, M. and Wiemann, S.
EST (Lauder, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.)
JOURNAL
Unpublished (2003)
COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the CDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZP781C0629) is available at the RZPD in Berlin.
Please contact the RZPD: Resourcenzentrum, Heuberg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source
1..839
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP781C0629"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="781 (synonym: h1cc4)"
/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb;
CDNA-collection"

ORIGIN

Query Match 35.9%; Score 419.8; DB 5; Length 839;
Best Local Similarity 74.1%; Pred. No. 3e-106;
Matches 546; Conservative 0; Mismatches 187; Indels 4; Gaps 1;
QY 8 CAATATACAGTACATGCCTTAACATCAATTAATTTCTTGACATTTTATGCTT 67

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Db      106 CTAATAGCACAATTCATTTATCACTAAGCAGCTGCTTCTTTAGCATTTTATGCTCT
Qy      68 TACTAGCTATGCTATTAATAGTAGGCAATGCTGGTCACTTTAGCTTTATTTGGAGA
Db      166 TAGTAGCTTTTCTATTAATGCTAGAGAAATGCTTTGGTCACTTTTGGTGGAGAA
Qy      128 GAAATCTTAGACATGCAATTAATCTTTTCTTAATCTTGGCCATTGAGACTTCTTGG
Db      226 AAAACCTTAGACATGCAATTAATCTTTTCTTAATCTTGGCCATTGAGACTTCTTGG
Qy      168 TGGGTGCAATTCGCAATTCCTCTGATACATCTTCTCGCTGCTTACTGAGCTTCTGAA
Db      286 TGGGTGATCTCCATTCCTTTGATACATCTTCTGACACGCTGTTGCAATGGGAATTTGGAA
Qy      248 AGCAAGCTTGATTTTGGCTCATCTAGCATCTTTTATGATGACAGCATCTGATATA
Db      346 AGGAATCTGATATTTTGGCTCACTAGCATCTTGTATGATACAGCATCTGATATA
Qy      308 ATATTGCTCTATCAAGCTACGATCGCTACAGTCAATGCGCTGTGTATAGAG
Db      406 ACATTGCTCTATCAAGCTACGATCGCTACAGTCAATGCGCTGTGTATAGAA
Qy      368 CTCAGCATCTGAGCAGCTGGAATTTGCTACTCAAGTGGTGGCTGTTGGATTTCTCT
Db      466 CTCACATACCTGGGGCTTGAAGATTTGCTGATGCTGCGCTGTTGGTGGCTGCT
Qy      428 TCATGACAAATGGGCGATGATTTGATTTGAGACTCTGGGAGAAATAGCATACAGAA
Db      526 TCTTAGTGAATGGGCAATGATTTAGTTCAGAGCTTTGGAAGATGAAGTAGTAAT
Qy      488 GTGAACCTGGATTTTAAAAAGTGTACTTGTCTCCCTACATCATTTATGGAATTC
Db      586 GTGAACCTGGATTTTTCGGAATGGATCCTTGGCCATCATCATCTTGGAAATTC
Qy      548 TGATCCCATCTTTTGTAGTGTCTTATTTAGGCGCCATTTACTGAGCTGTGGAAGC
Db      646 TGATCCCATCTTTTGTAGTGTCTTATTTCAACATGAATTTATGGAACCTGTGGAAGC
Qy      608 GAGAGAACTGAGCAGTGTCTCAGCAGCCTGTACTCTCCCTGTGATCTTTCAGAGAG
Db      706 GTGATCATCTCAAGTAGAGTCCAAAGCATCTGAGTCACTGTCTTCTTCAATCTG
Qy      668 ACCAGCAGCATCTCTGAGCAGACCCGCAATTCAGAGCGACTCTGCCAGCAGAAAG
Db      766 ---TGAACACTCATTTAGAGGTAGACTATCTTCAAGAGATCTCTTCTGATGACAG
Qy      728 AAACAATGCTCTCTT 744
Db      822 AAGTTCCTGATCTCTT 838

RESULT 2
CP147821      704 bp      mRNA      linear      EST 25-JUL-2003
DEFINITION   AGGCCOIRT_14740195 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:6971900 5', mRNA sequence.
ACCESSION   CP147821
VERSION     CP147821.1 GI:33244089
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 704)
NIH-MGC http://mhc.nci.nih.gov/
Unpublished (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)
CONTACT: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabds-r@mail.nih.gov
```

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Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB102 row: b column: 07
High quality sequence stop: 685.
FEATURES
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:6971900"
            /tissue_type="mixed"
            /lab_host="DH10B"
            /clone_idb="NIH_MGC_145"
            /note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',
5'-EcoRV-XmiI/XhoI-3', EcoRV (in cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/seqarrayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC library."

ORIGIN
Query Match      35.1%; Score 410.6; DB 7; Length 704;
Best Local Similarity 75.6%; Pred. No. 1.1e-103;
Matches 509; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

8 CAAATTAACAGTACATCGCCTTAACATCAATTAATTTCTTGAATTTAATGCTT 67
9 CTAATAGCAATTCATTTATTCATACAGACTCGCTTATAGCATTTTATGCTCT 68
68 TACTAGCTATGCTATTAATGTTAGCAATGTCGTGCTATTTAGCTTTATTTGGAGA 127
69 TAGTAGCTTTTGTCTAATAGCAGAAATGCTTGTGATTTTACTTTTGTGGAGAA 128
128 GAAATCTTAGACATGAAGTAATTTCTTTTCTTAATCTGGCCATTGCAACTTCTT 187
129 AAAACCTTAGACATGAAGTAATTTCTTTTCTTAATCTGGCCATTGCAACTTCTT 188
188 TGGGTGCAATTCGCAATTCCTGTATACATCTTCTGCTGCTTACTAGCACTTCGAA 247
189 TGGGTGATCTCCATTTCTTTGTAATCCTTCAACAGCTGTGCAATGGGAATTTGAA 248
248 AGCAAGCTTGATTTTGGCTCATCTAGTACTATCTTTATATGACAGCATCTGTATAT 307
249 AGGAATCTGATATTTTGGCTCACTAGCTATCTGTATATGACAGCATCTGTATATA 308
308 ATATTGCTCTATCAAGCTACGCTACCACTGCTCAATGCGCTGTGTATAGAG 367
309 ACATTGCTCTATCAAGCTACGCTACCACTGCTCAATGCGCTGTGTATAGAA 368
368 CTCAGCATCTGAGCAGCTGGAATTTGCTACTCAAGTGGTGGCTGTTGGATTTCTCT 427
369 CTCACATACCTGGGGCTTTGAAGATTTGCTTCTATAGTGGCCGTTTGGGTGGCTT 428
428 TCATGACAAATGGGCGATGATTCGATTTGAGACTCTTTTGGAGAAATAGCATACAGAT 487
429 TCTTAGTGAATGGGCAATGATTCGATTTGAGACTCTTTGGAAGATGAAGTAGTAAT 488
488 GTGAACCTGGATTTTAAAAAGTGTACTTGTCTCTCCCTCAATCATTTATGGAATTC 547
489 GTGAACCTGGATTTTTCGGAATGTGTACATCTTGGCCATCAATCATCTTGGAAATTC 548
548 TGATCCCATCTGTTAGTGTGCTTATTCAGGCGCCATTTACTGAGAGCTGTGGAAGC 607
549 TGATCCCATCTTGTAGTGTGCTTATTCACATGAATTTATTTGAGAGCTGTGGAAGC 608
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OY	608	GAGGAAACCTGAGCAGGTGGCCCTCAGACCACCGCTGTAATCCCGTACTTCACAGCACTG	667
Dd	609	GTATTATCTCATCTAGTAGTGTCGCCAAGACCATCTCTGAGTACTGCTCTCTTCCACATCTG	668
OY	668	ACCACGCAGCACTC	680
Dd	669	TGGACACTCATTTG	681
RESULT 3			
C0959034			
LOCUS	C0959034	721 bp	mRNA linear EST 17-AUG-2004
DEFINITION	AGENSCOURT 30842625 NIH MGC 146 Homo sapiens cDNA clone IMAGE:73189774 5' , mRNA sequence.		
ACCESSION	C0959034		
VERSION	C0959034.1	GI:51323616	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
	1 (bases 1 to 721)		
	NIH-MGC http://mgc.nci.nih.gov/.		
REFERENCE	National Institutes of Health, Mammalian Gene Collection (MGC)		
AUTHORS	Unpublished (1999)		
JOURNAL	Contact: Daniela S. Gerhard, Ph.D.		
COMMENT			

cdna library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINTL at:
<http://image.llnl.gov>
plate: IRB18 row: column: 04
high quality sequence start: 2
high quality sequence stop: 328.

FEATURES	Location/Qualifiers
Source	1. .721

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7389774"
/tissue_type="mixed"
/lab_host="RDH108 (T1-phage-resistant)"
/clone_lib="NIH_MGC_146"
/notes="vector: pcDNA3.1; Site 1: multiple; Site 2:
multiple; ORFs were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guttrrie cDNA Resource Center (www.guttrrie.org/cDNA)
into pcDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guttrrie
website, using the Guttrrie ID given in the file
http://image.lnl.gov/image\_rearranged\_plates/IRRF.presv.dat
". Note: this is a NIH_MGC Library."

```

Query Match	19.9%	Score 233	DB 7	Length 721
Best Local Similarity	74.6%	Pred. NO. 8e-54		
Matches 293; Conservative	0	Mismatches 100	Indels 0	Gaps 0

Qy	8	CAAAATACAGTACATCCGCTTAA	CATCAATTTAAATTTCTTGGACATTTTAAATGCTT	67
Db	32	CTAATAGCAATCAATTTATCAT	CTAGACATCGGTTACTTTAGCATTTTTTATGTCCT	91
Qy	68	TACATGCAATTTGCTATATGTTAG	CAATGTCGTCATTTTGGCTTTTATGTCACA	127
Db	92	TAGTACGCTTTTGCTATATGCTGA	AAATGCTTTGCTATTTTACCTTTTGGGTGGACA	151
Qy	128	GAAATCTTAGACATCGAAGTAA	TCTTTTCTTAACTTGACCATTCGACATTCCTTGG	187

D _b	152	AAAACCTTAACATCGAAGTAGTTATTTTTTTCTTAACCTTGGCCATCTCGACTCTTTG	211
Q _y	188	TGGGTGCAATTGCAAATTCCTCTGTACATPACTTCCTCGTACTCTACTGGAACCTTCGAA	247
D _b	212	TGGGTGTGATCTCCATTCCTTTGTACACCTTCAACAGCTGTTCGAATGGGAATTTTGGAA	271
Q _y	248	AGCAAGCTTGTGTATTTTGGCTCAATTAAGTACTATCTTTATGTACAGCATCTGTGTATA	307
D _b	272	AGGAAATCTGTGTATTTTGGCTCACTACTACATATCTGTATGTACCGGACGTGTATATA	331
Q _y	308	ATATTTCCTCATAGCTAGTACGATCGTACACGACGTCACTAAATGCGGTGTATAGAG	367
D _b	332	AGATTGTCTCATCGAGTATGATTAATAACTGTGTCATCTCAATTCCTTTGTATTAGGAA	391
Q _y	368	CTAGCACTCTGGCACTCGGAAAAATTTGTAATC	400
D _b	392	CGCAAAAAACGGGGGGGCTCTAAGAGGGGAACGC	424

RESULT 4	CD326085	853 bp	mRNA	linear	EST 28-MAY-2003
LOCUS	CD326085				
DEFINITION	AGAGNC00RT_14163426 NICHD_XGC_Eyel1 Xenopus laevis cDNA clone				
	IMAGE:6949081.5, mRNA sequence.				
ACCESSION	CD326085				
VERSION	CD326085.1	GI:31090416			
KEYWORDS	EST.				
SOURCE	Xenopus laevis (African clawed frog)				
ORGANISM	Xenopus laevis				

REFERENCE	1 (bases 1 to 853)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Daniela S. Gerhard, Ph.D.

JOURNAL
COMMENT

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabds-r@mail.nih.gov
Tissue Procurement:
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL14564 row: f column: 24
High quality sequence set: 707

FEATURES	Location/Qualifiers
Source	1. .853

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/mol_type="mRNA"
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/clone IMAGE:5949081"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NICHD XGC Eye1"
/note="Organ: eye; Vector: PCMV-SpOrt6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 2.3 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."

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ORIGIN

Query Match	10.94;	Score 127.8;	DB 6;	Length 853;
Best Local Similarity	58.64;	Pred. No. 2.9e-24;		
Matches 24;	Conservative	0;	Mismatches 167;	Indels 3;
			Gaps	1;
QY	50	TGACATTTAAAGTCCTTTACAGCAATTCCTAATGTAAGCAATGTCGTGATTT	109	

Db 389 TGGCTGCTGATGAGGGGCTCTCATAGTTCAGACCGGTGCGGAATGCCGTGATGC 448
Qy 110 TAGCTTTATTTGTGAGACAGAAATCTTAGACATGAGTAATTTCTTTCTTAAGTGG 169
Db 449 TGGCTTTTGTGTGAGATCTGACGCTCCGACCCAGAAATATTTCTTCTTCTGACCTGG 508
Qy 170 CCAATGACAGATCTTTTGTGGGTGCAATTCGATTTCTCTGATACATTTCTTCTGCTGA 229
Db 509 CTATCTCAGATTTCTTTGTAGGTGCGCTGTGATGATCCCTCTGATGTGCAATGACGTA 568
Qy 230 CTTC--TGACCTCTGGAAGACAGCTGTGTATTTTGTGCTATTAAGTCTTCTTT 286
Db 569 CTGGAGATGAGCTTTTGGCAGAGCGCTTTCGAACTGTGCTGTCTGATTAATCTGC 628
Qy 287 TATGACAGACATCTGTATTAATATTTCTTCATGAGTACAGATGCTACACGATGCT 346
Db 629 TCTGACCTCTGCTGCTGTTTCAACATCTGCTCATAGCTACAGACAGTTCACTCTGGA 688
Qy 347 CAAATGCCGTGTGTATAGCTCAGCACTGCGACCTGGAATTCCTACTCAGATGG 406
Db 689 CCGGCGCTGTGAGTACGAGCTCAGAGATGACAGCGCGCATGCTTGAATAAATGA 748
Qy 407 TGGCTGTTGATATTTCTTCATGACAAATGGCGCATGATTTCTGATTT 457
Db 749 CCATGCTGTGATCTTGGCTTTCTCTATATGACCAAGCCATTAATAT 799

RESULT 5
CB556920 672 bp mRNA linear EST 02-APR-2003
LOCUS AMGNND:UMGPI-00001-D6-A urgpi (14349) Rattus norvegicus cDNA clone
DEFINITION urgpi-00001-d6 5', mRNA sequence.
ACCESSION CB556920
VERSION CB556920.1 GI:29496320
KEYWORDS EST
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 672)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Place: 00001 row: d column: 6.

FEATURES
source
1..672
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="urgpi-00001-d6"
/clone_1ib="urgpi (14349)"
/note="Vector: pSPORT1; Rat GPCR library rearrayed
internal pSPORT vector"

ORIGIN
Query Match 9.6%; Score 112; DB 6; Length 672;
Best Local Similarity 56.4%; Pred. No. 7.5e-20;
Matches 230; Conservative 0; Mismatches 175; Indels 3; Gaps 1;

Qy 59 TAAATGCTTACTAGTATTTGTAATATTTAGGCAATGCTGTCATTTAGCTTTTA 118
Db 227 TCATGCGCTGCTCATCGTGGCCACGATCTGCGCAACGCGTGTGATGCTGCGCTTCG 296
Qy 119 TTGTGACAGCAATCTTAGACATCGAAGTAATTAATTTTCTTAAGTGGCATTCGAG 178
Db 297 TGGCGATTCGAGCTCCGACCCAGAACAACTTTCTTTGTGCTCAACCTGCGCATCTCG 356
Qy 179 ACTTCTTTGTGGGTGCAATTCCTCTGATACATACCTTCTCGCTGACTTAC--T 235

Db 357 ACTTCCTGTTGGGCTTCTGCAATCCATGTGATGCCATGTGCTGACCGGCCGTT 416
Qy 236 GGACTTCGGAAGCAAGCTTGTGATTTTGGCCATTAAGTACATCTTTATAGTACG 295
Db 417 GGACCTTGCGCGCGGCTCTGCAAGCTGTGGGTGTGATGACTTACTTGTGTGCT 476
Qy 296 CATCTGTATTAATATTTGCTTCATACGATTAAGTGTGACAGTCTTCAATGCGC 355
Db 477 CCGGCTTCAACATGTGATCTCATGACGTATGACCCGATTCCTGTCAGTCACTGAGCTG 536
Qy 356 TGTGATATAGCTTCAGACTCTGACCTGACCTGGAATTTCTACTATATGTGTGCTTT 415
Db 537 TCTCTTACAGGCGCCAGAGAGGAGGACAGAACCGGCGCTTCGGAATGACACTGTGT 596
Qy 416 GGATATTCCTCTCATGACAAATGGCGCATGATTTCTGATTTAGACT 463
Db 597 GGGTGTGCTGCTTCTGCTGTATGAGGCTGCTGCACTTCAAGTTGGAGT 644

RESULT 6
CF147822 732 bp mRNA linear EST 25-JUL-2003
LOCUS AGNCOURT.14740187 NIH_MGC_145 Homo sapiens cDNA clone
DEFINITION IMAGE:6971899 5', mRNA sequence.
ACCESSION CF147822
VERSION CF147822.1 GI:33244090
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 732)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: ggarbs-remail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: IRB102 row: b column: 06
High quality sequence stop: 610.

FEATURES
source
1..732
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971899"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_1ib="NIH MGC 145"

/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XbaI/XhoI-3',
5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clone represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Query Match 9.3%; Score 109.2; DB 7; Length 732;
Best Local Similarity 52.7%; Pred. No. 4.7e-19;
Matches 293; Conservative 0; Mismatches 248; Indels 15; Gaps 2;

QY 59 TAATGCTTACTAGTATGCTAATAATGTAAGCAATGTCGTGCTATTTAGCTTTTA 118
 DB 135 TCAATGCGCTGCTCATGCTGCGCCAGCGTGTGGCAACGGCGTGTCTATCTGCTTCG 134
 QY 119 TTGTGACAGAAATCTTGAACATGAGATTAATTTCTTTTCTTAACTTGGCCATTCAG 178
 DB 195 TGCCCACTGAGCTTCGCCAGAACCAATCTTCTGCTCAACCTGCCATCTCCG 254
 QY 179 ACTTCTTTGGTGGTGAATGCAATTCCTCTGTAACACTTCTGCTGAC---TTACT 235
 DB 255 ACTTCTCTGCGCGCTTCTGCACTGTAATGTAACCTTACCTGCTGACAGCGCT 314
 QY 236 GGAATTTCTGGAAGCAAGCTTGTGTAATTTGGCTCATTACTGACTATCTTTATGTAAG 295
 DB 315 GGAATTTCTGCGCGCGCTGCTGCAAGCTGTGCTGTAAGTGAATCTCTGCTGCACT 374
 QY 296 CATCTGTGTAATAATTTGCTCTCATGCACTAGATGCTACCAATGCTCAATGCGC 355
 DB 375 CCTGCTGCTTCAACATGCTGCTCATGCACTAGACGCGCTTCTGCTGCTGCAACGCG 434
 QY 356 TGTGTAATGAGCTGCACTGCGCACTGCAAAATTTGCTACTGATGCTGCTGTT 415
 DB 435 TCTCATACCGGCGCCAGAGGAGTGAACGCGCGCGGCAAGTCTGCTGCTGT 494
 QY 416 GGAATTTCTGCTGCACTGCAAAATGCGCGCATGTAATTTGCACTGCTGCAAGATA 475
 DB 495 GGAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 554
 QY 476 GCACTAC-----AGAAATGTAACCTGTAATTTTAAATGCTGCTGCTGCTGCT 523
 DB 555 GCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
 QY 524 TCCCTACATCATTTGGAATTCCTGATCCCATCTTGTGTAATTTGCTGTAATTTG 583
 DB 615 TCAACGCTTCCACAGCTGAGTCTTTACGCGCTTCTGCAAGCTGCTGCTGCTGCT 674
 QY 584 ATATTACTGAGAGCT 599
 DB 675 CCATCTACCTGAACAT 690
 RESULT 7
 CC481311 684 bp DNA linear GSS 16-JUN-2003
 LOCUS CH240_309C10.77 CHORI-240 Bos taurus genomic clone CH240_309C10,
 DEFINITION genomic survey sequence.
 ACCESSION CC481311
 VERSION CC481311.1 GI:31760574
 KEYWORDS GSS.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 1 (bases 1 to 684)
 Holt, R., Scott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
 Tsai, M., Cloutier, A., Lee, D., Gilm, N., Olson, T., Mayo, M.,
 Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A.,
 Matheson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,
 Schein, J., Marra, M., de Jong, P., McMillan, S., Barris, W.,
 Dalrymple, B. P. and Tellam, R.
 Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
 Unpublished (2003)
 Other GSSs: CH240_309C10.TABRAC13P2
 Contact: Rob Holt
 TITLE The British Columbia Cancer Agency Genome Science Centre
 JOURNAL Sequencing
 COMMENT The British Columbia Cancer Agency Genome Science Centre
 600 W. 10th Ave. Vancouver, British Columbia, Canada V5Z 4E6
 Tel: 604-877-6085
 Fax: 604-877-6276
 Email: rholt@bccsc.ca
 Clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/bacpac/bovine240.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering/information.htm). This work
 was undertaken as part of the International Bovine BAC Mapping
 Consortium (IBMC) by CSIRO Livestock Industries, Australia and the
 British Columbia Genome Sciences Centre, Canada.
 Plate: 309 row: C column: 10
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
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 /db_xref="taxon:9913"
 /clone="CH240_309C10"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="CHORI-240"
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
 Hereford bull LI Domino 99375; CHORI-240 Bovine BAC
 library (Male) produced by Pieter de Jong"

ORIGIN
 Query Match 8.9%; Score 104.4; DB 9; Length 684;
 Best Local Similarity 67.4%; Pred. No. 16-17;
 Matches 147; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 147 TAATTAATTTTCTTAACTGCGCATGTCAGACTTCTTTGGTGCATTCGAATTC 206
 DB 260 TAGGTGTAATTTGTAATCTTCAATTTTTCGCCCAAGAGTATGATCCATTC 319
 QY 207 TCTGTACATACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 266
 DB 320 TTATATCATCCCTCAACAGCTCTTCAACGAGTTGAAATTAACATTTGTGCTTTG 379
 QY 267 GCTCATTAAGTATCTTTTATGTAAGCATGTAATTAATTTGCTCATGAGCTA 326
 DB 380 GCTCACTACTGATTAATTTTGTGTAAGCATGTAATTAATTTGCTCATGAGCTT 439
 QY 327 CGATGCTACAGTCAAGTCAATGCGGTGTGATA 364
 DB 440 TGATGATATCACTGCTCAATGCTGTAATCAAA 477
 RESULT 8
 AL848045 643 bp mRNA linear EST 26-NOV-2003
 LOCUS AL848045 XGC-egg Xenopus tropicalis cDNA clone TEG9022122 5', mRNA
 DEFINITION sequence.
 ACCESSION AL848045
 VERSION AL848045.2 GI:38559584
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenophodinae; Xenopus; Silurana.
 1 (bases 1 to 643)
 Croning, M.D.R., Ahnuc, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
 Sanger Xenopus tropicalis EST project 2001 (11_2003)
 Unpublished (2003)
 On Sep 15, 2002 this sequence version replaced gi:22868310.
 Contact: Taylor R
 Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS_SEQUENCE_ID: TEG9022122.pl1SP6
 Sequencing primer: SP6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.

CDNA was oligo dT primed from 5 μ g of poly A⁺ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: *Escherichia coli* XL1-blue.

FEATURES
SOURCE

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/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="rEG9022122"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="Xgc-egg"
/note="Vector: pCS107, Site_1: EcoRI, Site_2: NotI, cDNA
was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"

```

ORIGIN

Query Match	7.4%	Score 86;	DB 1;	Length 643;
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Qy	190	GGTGCMAATTGCATTTCCTCTGTACACTACCTTCTCGTGACT---TACTGCACCTTCTGGA	246
Db	83	GGTGGATTCTGCATCCCACTCTAATATCCCTTAATGTGCTGACTGGCCAGGTGGAAGTTTGGG	142
Qy	247	AAGCAAGCTTGATGTATTTTGGCTATTACTGACTATCTTTTATGTACAGCAATCTGTAT	306
Db	143	AAAGGCTTGTCGAACCTTGTGGCTAATATATGACACTACCTTTTATGACACGTGCTTCACTTTT	202
Qy	307	AATATGTTCCTCATAGCTACGATGCGTACCAAGTCAGTCTCAATATGCCGTGTGTATAGA	366
Db	203	AATATGTTCCTCATAGCTATGACAGGTTCATCTCAGTACACTAAAGCCGTGTCTTACAGA	262
Qy	367	GCTCAGCACTCTGGCACCCTGGAAATTTGCTACTCAGATGGTGGCTTTGGATATTTCCTC	426
Db	263	GCACAGAAAGGAATACCAAGAAATCAGATGTTAAATATGCTTATTTGTTGGGTGGCAGCC	322
Qy	427	TTTCATGACAAATGGGCGGATGATTTCTGATTTTCAGACTCTTGGCAGAAATAGCACTA----	481
Db	323	TTTCTTCTCTATGGCCCAAGCCATCTATCTACCTGGGAATCAATGCAAGAATCTACTTCTTA	382
Qy	482	-----CAGATGTGAACCTGGATTTTAAAAAAGGTGACTTGTGCTCTCCCTTACATCA	534
Db	383	CCAGAGGGGAAATGTTATGTATGAATTTCTACTCAACTGATATTTCTGATGATAGCTTCC	442
Qy	535	TTATTTGGAATTCCTGATCCCATCTTTGTATGTGCTTATTTTCAGGCCCATATTTTACTCG	594
Db	443	ACAATAGAAATCTTATCTCACTTCATCAAGTGTATTACTTTCATATCTAAGCATCTACATT	502
Qy	595	AGCCTGTGAAGCGAGAGAAACTGACGA	622
Db	503	AACATCAAAAGAGAACTATGATGGAA	530

RESULT 9	
B567596	
LOCUS	BE567596
DEFINITION	499 bp mRNA linear EST 12-DEC-2000 UI-R-B00-agr-c-06-0-UI r1 UI-R-B00 Rattus norvegicus cDNA clone UI-R-B00-agr-c-06-0-UI 5', mRNA sequence.

discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED 97044477
8889548
Contact: Soares, MB
COMMENT

FEATURES
source

Location/Qualifiers
1. .499

ORIGIN

Query Match	7.1%	Score 83.2	DB 2	Length 499
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OY	189	GGGGGCAATTGCATTTCTCTGTACATACACTTCCCTCGGACATAC---TGGACTCTGG	245
Dd	58	GGGTGCTCTTCGATCCATTCGATGACGACCTTATGTGCTGACCGGCCGTTGGACCTTCGG	117
OY	246	AAAGCAACCTTGATGATTTTGGCTCATTAAGTACTATCTTTATGACAGCAATCTGTGTA	305
Dd	118	CCGGGGGCTCTGCAAGCTGTGGCTGTGGTGAACTAACCTACTGTGTGCTCTCGGATCTT	177
OY	306	TAAATATGTTCTTCATCAGCTACGATGCGTACCAAGTCAGTCTTCAAAATGCCGTGTGGTAAG	365
Dd	178	CAACATGTACTCATACACGTAATGACCGAATTCCTGTCAAGCATCTGAGCATCTGTCTCTACAG	237
OY	366	AGCTCAGACTCTGGCACCCTGGAATAATGTAAGTACTAGATGTGTGGCTGTTGGATATTTCTC	425
Dd	238	GGCCGAGAGGGGGGACAGAGACGGGCCGTTTCGAAAGATGGCACTGTGTGGGTGCTGGC	297
OY	426	CTTCATGACAAATGGGCGCGATGATTCGATTTCAACACTTTGGCAGAATAGCATAC---	482
Dd	298	CTTCTGTGTGTAATGGGCTTGCATTCCTAGATTGGAGTAACCTGTCTGTGGGCGATTCAT	357
OY	483	-----AGAAATGTGAACCTGATTTTAAAAAAGTGTACTTTGCTCTCCCTCATATC	533
Dd	358	CCCCGAGGGCCACTGTCTATGCTGAATCTTTCTTACAACGTGTACTTTCTATACGAGNCTC	417
OY	534	ATTATTTGAATTCCTGATGCCCATCTGTATGTTGCTTATTTCAAGGCCCATATTTACTG	593
Dd	418	CACCTCGAGTTCTTACAGCCCTTCTCAGGCTTACAGGTTACCTTTCAACCTCAGACTTACCT	477
OY	594	GAGCCTGTGAAGCG	608

Db	478	GAACATCCAGAGCGC	492
RESULT 10	CNS03296	921 bp	DNA
LOCUS	CNS03296/c		
DEFINITION	Tetraodon nigroviridis genome survey sequence T7 end of clone 206D09 of library G from Tetraodon nigroviridis, genomic survey sequence.		
ACCESSION	AL224547	GI:7883412	
VERSION	AL224547.1		
KEYWORDS	GSS: genome survey sequence.		
SOURCE	Tetraodon nigroviridis		
ORGANISM	Tetraodon nigroviridis		
REFERENCE	1 Roest Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzmes,C., Winkler,P., Brotlier,P., Quetier,F., Saurin,W. and Weissbach,J.		
AUTHORS	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis		
TITLE	Genome Res. 10 (7), 939-949 (2000)		
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)		
MEDLINE	20296633		
PUBMED	10835645		
REFERENCE	2		
AUTHORS	Roest Crolius,H., Jallion,O., Dasilva,C., Ozouf-Costaz,C., Fitzmes,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissbach,J.		
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis		
JOURNAL	Genome Res. 10 (7), 939-949 (2000)		
MEDLINE	20359837		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
MEDLINE	10899143		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
MEDLINE	10899143		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
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TITLE	Direct Submission		
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MEDLINE	10899143		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
MEDLINE	10899143		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
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TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
MEDLINE	10899143		
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REFERENCE	3 (bases 1 to 921)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
MEDLINE	10899143		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
MEDLINE	10899143		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
MEDLINE	10899143		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
MEDLINE	10899143		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
MEDLINE	10899143		
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REFERENCE	3 (bases 1 to 921)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
MEDLINE	10899143		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
MEDLINE	10899143		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
MEDLINE	10899143		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
MEDLINE	10899143		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
AUTHORS			

Db		412	CCCTTCTGTAACCGCGTGTCGCACAGAGCCTTCGGAGGGCTTTCTCCAATCTCTGT	353
Oy	1123	GTCGAGAAGCAATCCACGCCACACACAAC	1152	
B7728212				
DEFINITION	BY728212	RIKEN full-length enriched, adult male corpus striatum Mus musculus cDNA clone C030026Cg2.5, mRNA sequence.		
ACCESSION	BY728212	GI-27141339		
VERSION	EST.	Mus musculus (house mouse)		
SOURCE	Mus musculus	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
ORGANISM	AUTHORS	Okazaki,Y., Furuno,M., Kaeukawa,T., Adachi,J., Bono,H., Kondo,S., Nikiato,I., Osaeto,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yeigi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult.C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,A., Brad,D., Brusic,V., Clotcher,C., Corbani,L.E., Cousins,S., Dalla,E., Draganji,T.A., Fletcher,C.F., Forrest,A., Fraser,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmel,S., Gusticlich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kanaaj,H., Kawasawa,Y., Kedzierka,R.M., King,B.L., Konagaya,A., Kirochikhi,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Nunata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Rिंगwld,M., Sandelin,A., Schneider,C., Sample,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tonit,M., Vearato,R., Wagner,L., Wahlenstedt,C., Wang,Y., Wetanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagiisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu.Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Kono,H., Nakamura,M., Sakazume,N., Satoh,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Atakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishi,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shigaenaw,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.		
TITLE	JOURNAL MEDLINE PUBMED	Nature 420, 563-573 (2002)		
COMMENT	12466851	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Sehitcho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@sc.riken.jp, URL:http://genome.gsc.riken.jp/ Adechi,J., Aizawa,K., Akimura,T., Arakawa,T., Carncini,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Horii,F., Imotani,K., Ishi,Y., Itoh,M., Kagawa,I., Kawai,J., Koituma,Y., Kondo,S., Kono,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numasaki,R., Ohno,M., Ohnato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watanishi,A., Muramatsu,M. and Hayashizaki,Y.		
		Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)		
		Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new		

QY	245	GAAGCAAGCTGTTGATATTTGGSCATTAACGACTATCTTTATGTACAGATCTGT	304
Db	279	GCACATGGCCCTGATACCTCTGGCTGGCCCTGGACTATATGTGGCCAGCAACGCTCTGTCA	338
QY	305	ATAATATATGCTCTATCATGATACGATCGCTACCACTCAGTCTCAATAATCCGTTGGTATA	364
Db	339	TGAATCTTCTGTCTATCATGCTTTTGAACCTTACTTCTCAGTAGACCGACCCCTGACTAC	398
QY	365	GAGCTCAGCACTCTGGCACTGG	387
Db	399	GAGCCAAAGCGACATCCCGCAGG	421
RESULT 13			
LOCUS	BI757352		
DEFINITION	603025570P1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5199905 5',	940 bp, mRNA	linear EST 25-SEP-2001
ACCESSION	BI757352		
VERSION	BI757352.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 940)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strusberg, Ph.D.		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 940)	NIH-MGC	http://mgc.nci.nih.gov/ .	National Institutes of Health, Mammalian Gene Collection (MGC)	
		Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.			
	Email: cgabbs-remail.nih.gov			
	Tissue Procurement: Life Technologies, Inc.			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LNL at:			
	http://image.lnl.gov			
	Plate: LNA11500	row: 1	column: 18	
	High quality sequence stop: 865.			

FEATURES	Location/Qualifiers
source	1. .940

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/mol_type="mRNA"
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/clone_1fb="NIH_MGC_114"
/notes="Organ: brain; Vector: pCMV-Sport6; Site 1: Notif; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

```

ORIGIN

Query Match	6.4%	Score 75	DB 4	Length 940
Best Local Similarity	52.7%	Pred. No. 2e-09		
Matches 187, Conservative		0, Mismatches 165,	Indels 3,	Gaps 1,

[illegible]

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RESULT 14	
AK081248	
LOCUS	3816 bp
DEFINITION	Mus musculus adult male corpus striatum cDNA, RIKEN full-length enriched library, clone: C03026622 product: MOSCAINIC ACETYLCHOLINE RECEPTOR M1, full insert sequence.
ACCESSION	AK081248
VERSION	AK081248.1 GI:26349070
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED
1	Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning Meth. Enzymol.	303, 19-44 (1999)	99279253	
2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,				10349636

TITLE
Itoh, N., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159

REFERENCE
AUTHORS
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Komno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishite, T., Harada, A., Yamamoto, R., Matsumoto, H., Sekiguchi, S., Ikegami, T., Kashiwagi, K., Fujimoto, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Maruyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE
RIKEN integrated sequence analysis (RISA) system—384-format
sequencing pipeline with 384 multicapillary sequencer

JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)

PUBMED
11076861

REFERENCE
AUTHORS **4** **The RIKEN Genome Exploration Research Group Phase II Team and the**

TITLE	JOURNAL	REFERENCE
PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection	Nature 409, 685-690 (2001)	5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE	Analysis of the mouse transcriptome based on functional annotation
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 3816)
AUTHORS	Miyajima T, Yoshida T, Kamei Y, Shimizu T, Kamei T, Carninci P

AUCHINCLOSS, J., ALZAGUA, R., HAMMILL, L. F., BOLAN, C., CALHOUN, E. A.,
FUKUDA, S., FUJINO, M., HANAGATA, T., HARA, A., HASHIZUME, W.,
HAYASHIDA, K., HAYATSU, N., HIROKAWA, K., HIRAKAWA, T., HISAKANE, T.,
HOTI, F., IMOTANI, K., ISHII, Y., ITOH, M., KISIKAWA, I., KASUKAWA, T.,
KATO, H., KAWAI, J., KOJIMA, Y., KONDO, S., KOMO, H., KOUDE, M.,

TITLE
JOURNAL

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ono, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

COMMENT

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/
URL: http://phantom.gsc.riken.jp/
Location/Qualifiers

FEATURES
source

CDS

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ORIGIN

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Best Local Similarity 54.2%; Pred. No. 3.2e-09;
Matches 175; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

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DB TTGGCACTTCTTCACGAACCTCTATACCAACATACCTGCTCATGGCCACTGGCTCTG 461
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DB GCACTGAGCTGTGACTCTGTGCTGAGCTGAGCTGATGTGAGCCAGCAAGCTCTGTGA 521

305 ATAAATATGCTCTCATCAGTACGATCGTACCAAGTCTCAATGCCGTGTGTATA 364
DB TGAATCTTCTGCTCATACGCTTTGACCGCTTACTTCTGATGACCGGACCCGACTACC 581
365 GAGCTCAGCACTCTGGCAGCTGG 387
DB GAGCCAGCGACGACCTCCCGCAGG 604

RESULT 15

LOCUS CO138455 700 bp mRNA linear EST 17-JUN-2004
DEFINITION EST833126 Aspergillus flavus Normalized cDNA Expression Library
Aspergillus flavus cDNA clone NAFCR84 5' end similar to (CA849238)
SI:234G2.4 (Novel protein similar to human histamine receptor H3
(HRH3)) mRNA sequence.

ACCESSION CO138455
VERSION CO138455.1 GI:48887433
KEYWORDS EST.
SOURCE Aspergillus flavus
ORGANISM Aspergillus flavus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 700)
Yu, J., Whitelaw, C.A., Nieman, W.C., Bhattacharya, D. and Cleveland, T.E.
Aspergillus flavus expressed sequence tags for identification of
genes with putative roles in aflatoxin contamination of crops
FEMS Microbiol. Lett. (2004) In press

CONTACT: Yu J
Food and Feed Safety Research Unit
USDA/ARS, Southern Regional Research Center
1100 Robert E. Lee Boulevard, New Orleans, LA 70124, USA
Tel: 504 286 4405
Fax: 504 286 4419
Email: jinyu@rrc.ars.usda.gov
Contact Dr. Yu at USDA/ARS SRRC (jinyu@rrc.ars.usda.gov) for clone
information
PCR Primers
FORWARD: M13F
BACKWARD: M13R
Seq primer: M13 Forward
POLYA=No.

JOURNAL
COMMENTFEATURES
source

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ORIGIN

Query Match 6.4%; Score 74.8; DB 7; Length 700;
Best Local Similarity 60.1%; Pred. No. 2.1e-09;
Matches 143; Conservative 0; Mismatches 92; Indels 3; Gaps 1;

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DB AACTATCATGACAGGAAGTTGCAAGTCACTTGCATATTTGTGTGCTTTGCA 217

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Qy 1001 TGACTAAATCAACCTGGTACCAATGCTTTGGCTCCAGTGTCAATTCCTTTGTTA 1060
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Db 275 GTGTCATTCAAGTCTCTATCAAAATTAACCTTTGGCTTTGTGATCAATTCCTCTGA 334
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Qy 1061 ATCCCTTTTGTATTCATGTGTGACAAAGCTTTTCAGAAAGCTTTCGAAATTAAT 1118
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 Job time : 3589 secs

Page Mark (usps)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 01:48:33 ; Search time 159 Seconds
(without alignments)
953.192 Million cell updates/sec

Title: US-10-626-398-10

Perfect score: 2036

Sequence: 1 MLANNSTIALTSIKISLFTL.....LKILPVROSTPPHNRISIST 389

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2036	100.0	389	US-10-626-445-10	Sequence 10, Appl
2	2036	100.0	389	US-10-626-126-10	Sequence 10, Appl
3	2036	100.0	389	US-10-626-398-10	Sequence 10, Appl
4	1308.5	64.3	390	US-09-812-216-2	Sequence 2, Appl
5	1308.5	64.3	390	US-09-910-411-2	Sequence 2, Appl
6	1308.5	64.3	390	US-09-875-076-14	Sequence 14, Appl
7	1308.5	64.3	390	US-09-876-252-14	Sequence 14, Appl
8	1308.5	64.3	390	US-09-852-165-2	Sequence 2, Appl
9	1308.5	64.3	390	US-09-891-138A-6	Sequence 6, Appl
10	1308.5	64.3	390	US-10-052-193-2	Sequence 2, Appl
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14	1308.5	64.3	390	US-10-393-807-14	Sequence 14, Appl
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21	1308.5	64.3	390	US-10-626-445-2	Sequence 2, Appl
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30	1236.5	60.7	391	US-10-626-445-9	Sequence 9, Appl
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41	689.5	33.9	445	US-10-727-021-7	Sequence 7, Appl
42	689.5	33.9	445	US-10-757-263-132	Sequence 132, App
43	689.5	33.9	445	US-10-735-963-1	Sequence 1, Appl
44	689.5	33.9	453	US-09-891-053-20	Sequence 20, Appl
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ALIGNMENTS

RESULT 1
US-10-626-445-10
; Sequence 10, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Cavia porcellus
; US-10-626-445-10

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Best Local Similarity 100.0%; Pred. No. 7.1e-170;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-10-626-126-10
Sequence 10, Application US/10626126
Publication No. US20050074770A1
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtypes
FILE REFERENCE: PRD-0033
CURRENT APPLICATION NUMBER: US/10/626,126
PRIORITY FILING DATE: 2003-07-23
PRIORITY APPLICATION NUMBER: 09/790,849
PRIORITY FILING DATE: 2001-02-22
PRIORITY APPLICATION NUMBER: 60/208,260
PRIORITY FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 389
TYPE: PRT
ORGANISM: Cavia porcellus
US-10-626-126-10

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Query Match	100.0%;	Score 2036;	DB 17;	Length 389;
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Db 361 CHKRFOKAFKLIPVRRQSTPPHNRISIST 389

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RESULT 3
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; Sequence 10, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DnaS Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 389
; TYPE: prt
; ORGANISM: Cavia porcellus
US-10-626-398-10

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Query Match	100.0%;	Score 2036;	DB 17;	Length 389;
Best Local Similarity	100.0%;	Pred. No. 7.1e-170;		
Matches 389;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0.

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Db	1	MLANNSTIALTSIKISLSTETMLSLAIAMLMGNVVIIAFIDYRNLRRHSNFFPLNLAIAD	60
QY	61	FFVGAIAIPLYIPSSLTWTWTSGRQACVFELLIDYLLCTASVYNIYLLSYDRYQGSNAVM	120
Db	61	FFVGAIAIPLYIPSSLTWTWTSGRQACVFELLIDYLLCTASVYNIYLLSYDRYQGSNAVM	120
QY	121	YRAQHSQGWKIAQOVAVMIISFPMNNGPMILISDSMNSTTECEBGLKKVYFALPTSL	180
Db	121	YRAQHSQGWKIAQOVAVMIISFPMNNGPMILISDSMNSTTECEBGLKKVYFALPTSL	180
QY	181	EPILPILVAVFSAHLYWSLKMREKLSRCLSHPVLPDSSSSDHGHSQRODPDSRATLPA	240
Db	181	EPILPILVAVFSAHLYWSLKMREKLSRCLSHPVLPDSSSSDHGHSQRODPDSRATLPA	240
QY	241	RKETTASLQSDKSRKRSLLPSIRAYKNSNVIASKQGLSHSDSLALQOREHIELFRARK	300
Db	241	RKETTASLQSDKSRKRSLLPSIRAYKNSNVIASKQGLSHSDSLALQOREHIELFRARK	300
QY	301	LAKSLAILLAAFAICWAPYSLTTVYISFEPBERNLTKSTWYHTAFLWQNFSPVNPFLYPL	360
Db	301	LAKSLAILLAAFAICWAPYSLTTVYISFEPBERNLTKSTWYHTAFLWQNFSPVNPFLYPL	360
QY	361	CHRRFOAKAPLILPVROSTPPHNSISIR	389
Db	361	CHRRFOAKAPLILPVROSTPPHNSISIR	389

RESULT 4
US-09-812-216-2
; Sequence 2, Application US/09812216
; Publication No. US20020098539A1

APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Laz, Thomas M.
APPLICANT: Monsuma, Frederick J. Jr
APPLICANT: Morse, Kelley L.
APPLICANT: Umland, Shelby P.
APPLICANT: Wang, Suke

TITLE OF INVENTION: Histamine receptor
FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/414,010
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-09-812-216-2

Query Match 64.3%; Score 1308.5; DB 9; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106; Indels 3; Gaps 3;
Matches 252; Conservative 48; Mismatches 84;

QY 5 NSTIALT-SIKISLTFELMSLAIAMGNVVLAFIVDRNLHRNSYFELNLAIDFEV 63
DB 5 NSTINSLSTRVTLAFPMGLVAFALMGNALVILAFVDRNLHRNSYFELNLAIDFEV 64
QY 64 GAIAPLYIPSSITWTSGKQACVFWLITDYLLCTASVNIIVLISYDRYQSVSNAVYRA 123
DB 65 GVASISLYIPHTLFEWDFGKEICVFWLITDYLLCTASVNIIVLISYDRYLSVNAVSYRT 124
QY 124 QHSGTKIKTQWAAVAFISFMTNGPMILISDSQNSSTCEPGLFKWYFALPTSLLEFL 183
DB 125 QHTGVAKITVLWAAVAVLAFVNGPMILVSESKDGSCEPGEFSEWYILAITSLFEV 184
QY 184 IPIILVAFSAHIYMSLMKREKLSRCLSHPVLPSSDSSDHGSCRODPDSRATLPARKE 243
DB 185 IPIILVAFYNNMIYMSLMKRDHLSRCQSHGLTA-VSSNICHSFGRSLSRSLASTB 243
QY 244 TIASLGSXSRKSSILPSIRAYKSNVIAKMGFLSHSDSLAQREHIELFRARKLAK 303
DB 244 VPASFSESRQRKSSIMFSSRTQNSNTIASKMGFSQSDSVALLHOREHVELLRARLAK 303
QY 304 SLATILAAFAICAPYSLTTVIYSFPERNLTKSTYHNAFWLQWNSFVNPLYPLCHK 363
DB 304 SLATILGVAVCAVPYSLFTVIYSFYSATGPKSVWYRIAFLWQNSFVNPLYPLCHK 363
QY 364 RFQKAFKILPVROQSTP-PHNRISIT 389
DB 364 RFQKAFKILFCIKQPLPSQHSRVS 390

RESULT 5
US-09-910-411-2
Sequence 2, Application US/09910411
Patent No. US20020137054A1
GENERAL INFORMATION:
APPLICANT: Bergema, Derek
APPLICANT: Fitzgerald, Laura
APPLICANT: Li, Xiaolong
APPLICANT: Michalovich, David
APPLICANT: Zhu, Yuan
TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
FILE REFERENCE: GP70655-2C1
CURRENT APPLICATION NUMBER: US/09/910,411
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 09/693,761
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/431,898
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens

US-09-910-411-2

Query Match 64.3%; Score 1308.5; DB 9; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106; Indels 3; Gaps 3;
Matches 252; Conservative 48; Mismatches 84;

QY 5 NSTIALT-SIKISLTFELMSLAIAMGNVVLAFIVDRNLHRNSYFELNLAIDFEV 63
DB 5 NSTINSLSTRVTLAFPMGLVAFALMGNALVILAFVDRNLHRNSYFELNLAIDFEV 64
QY 64 GAIAPLYIPSSITWTSGKQACVFWLITDYLLCTASVNIIVLISYDRYQSVSNAVYRA 123
DB 65 GVASISLYIPHTLFEWDFGKEICVFWLITDYLLCTASVNIIVLISYDRYLSVNAVSYRT 124
QY 124 QHSGTKIKTQWAAVAFISFMTNGPMILISDSQNSSTCEPGLFKWYFALPTSLLEFL 183
DB 125 QHTGVAKITVLWAAVAVLAFVNGPMILVSESKDGSCEPGEFSEWYILAITSLFEV 184
QY 184 IPIILVAFSAHIYMSLMKREKLSRCLSHPVLPSSDSSDHGSCRODPDSRATLPARKE 243
DB 185 IPIILVAFYNNMIYMSLMKRDHLSRCQSHGLTA-VSSNICHSFGRSLSRSLASTB 243
QY 244 TIASLGSXSRKSSILPSIRAYKSNVIAKMGFLSHSDSLAQREHIELFRARKLAK 303
DB 244 VPASFSESRQRKSSIMFSSRTQNSNTIASKMGFSQSDSVALLHOREHVELLRARLAK 303
QY 304 SLATILAAFAICAPYSLTTVIYSFPERNLTKSTYHNAFWLQWNSFVNPLYPLCHK 363
DB 304 SLATILGVAVCAVPYSLFTVIYSFYSATGPKSVWYRIAFLWQNSFVNPLYPLCHK 363
QY 364 RFQKAFKILPVROQSTP-PHNRISIT 389
DB 364 RFQKAFKILFCIKQPLPSQHSRVS 390

RESULT 6
US-09-875-076-14
Sequence 14, Application US/09875076
Publication No. US20030017528A1
GENERAL INFORMATION:
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/141,448
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/156,653


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QY 5 NSTIALT-SIKISLTFELMSLAIAMGNVVLAFVDRNLRRNSYFFLNLAIADFFV 63
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Db 5 NSTINISLSTRVTLAFPMSLVAFAMGNALVTLAFVDRNLRRNSYFFLNLAIADFFV 64
QY 64 GAIAIPLYIPSSLTFTWTSKQACVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYWYRA 123
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 64 GAIAIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYSYRT 124
QY 124 QHSGTWKIATQWAVVIFSFMTNGPMILISDSQWNTTECEBPGLKKWYFALPTSLEFL 183
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 124 QHSGTWKIATQWAVVIFSFMTNGPMILISDSQWNTTECEBPGLKKWYFALPTSLEFL 184
QY 184 IPVLVAFYFMNNTIYMSLWKRDLHSLRCQSHDGLTA-VSSNICGHSFRGLSSRSLASTE 243
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 184 IPVLVAFYFMNNTIYMSLWKRDLHSLRCQSHDGLTA-VSSNICGHSFRGLSSRSLASTE 243
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RESULT 8
US-09-852-165-2
; Sequence 2, Application US/09852165
; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Land, Peter
; APPLICANT: Sejilicz, Torsten
; APPLICANT: Vogel, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030032784A1 G Protein-Coupled Receptors
; FILE REFERENCE: 00231regUS
; CURRENT APPLICATION NUMBER: US/09/852,165
; PRIOR FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USSN 60/203,108
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-165-2
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Query Match 64.3%; Score 1308.5; DB 10; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFELMSLAIAMGNVVLAFVDRNLRRNSYFFLNLAIADFFV 63
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 5 NSTINISLSTRVTLAFPMSLVAFAMGNALVTLAFVDRNLRRNSYFFLNLAIADFFV 64
QY 64 GAIAIPLYIPSSLTFTWTSKQACVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYWYRA 123
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 64 GAIAIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYSYRT 124
QY 124 QHSGTWKIATQWAVVIFSFMTNGPMILISDSQWNTTECEBPGLKKWYFALPTSLEFL 183
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 124 QHSGTWKIATQWAVVIFSFMTNGPMILISDSQWNTTECEBPGLKKWYFALPTSLEFL 184
QY 184 IPVLVAFYFMNNTIYMSLWKRDLHSLRCQSHDGLTA-VSSNICGHSFRGLSSRSLASTE 243
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 184 IPVLVAFYFMNNTIYMSLWKRDLHSLRCQSHDGLTA-VSSNICGHSFRGLSSRSLASTE 243
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QY 244 TTASLGSDDRKRSLLPSIRAYKSNVJASXKGFSLSHSDSLAQOREHIELEFRARKLAK 303
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Db 244 VPASFSHERQRKRSLLMFSSRTKMSNTIASXKGSFSQSDSVALHQREHIELEFRARKLAK 303
QY 304 STAILLAAPALICAPYSLTFTVYSFPERNLTKSTYHTAFWLQWNSFVNPLLYPLCHK 363
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 304 STAILLGVAVCAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPLCHK 363
QY 364 RFOKAFKILFVRROSTP--PHNRSIST 389
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 364 RFOKAFKILFCTIKQPLPSQHSRVS 390
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RESULT 9
US-09-891-138A-6
; Sequence 6, Application US/09891138A
; Publication No. US20030083245A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Daniel Chi-Hong
; APPLICANT: Zhao, Jiaqiang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030083245A1 GPCRs
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-6
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Query Match 64.3%; Score 1308.5; DB 10; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFELMSLAIAMGNVVLAFVDRNLRRNSYFFLNLAIADFFV 63
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 5 NSTINISLSTRVTLAFPMSLVAFAMGNALVTLAFVDRNLRRNSYFFLNLAIADFFV 64
QY 64 GAIAIPLYIPSSLTFTWTSKQACVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYWYRA 123
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 64 GAIAIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYSYRT 124
QY 124 QHSGTWKIATQWAVVIFSFMTNGPMILISDSQWNTTECEBPGLKKWYFALPTSLEFL 183
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 124 QHSGTWKIATQWAVVIFSFMTNGPMILISDSQWNTTECEBPGLKKWYFALPTSLEFL 184
QY 184 IPVLVAFYFMNNTIYMSLWKRDLHSLRCQSHDGLTA-VSSNICGHSFRGLSSRSLASTE 243
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 184 IPVLVAFYFMNNTIYMSLWKRDLHSLRCQSHDGLTA-VSSNICGHSFRGLSSRSLASTE 243
QY 244 TTASLGSDDRKRSLLPSIRAYKSNVJASXKGFSLSHSDSLAQOREHIELEFRARKLAK 303
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 244 VPASFSHERQRKRSLLMFSSRTKMSNTIASXKGSFSQSDSVALHQREHIELEFRARKLAK 303
QY 304 STAILLAAPALICAPYSLTFTVYSFPERNLTKSTYHTAFWLQWNSFVNPLLYPLCHK 363
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 304 STAILLGVAVCAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPLCHK 363
QY 364 RFOKAFKILFVRROSTP--PHNRSIST 389
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 364 RFOKAFKILFCTIKQPLPSQHSRVS 390
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RESULT 10

```
US-10-052-193-2
; Sequence 2, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-052-193-2

Query Match      64.3%; Score 1308.5; DB 13; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTLT-SIKSLTFELMSLAIATMLGNVVITAFIYDRNRHRSNFFELNLAIDPFV 63
DB 5 NSTILSLSTRVTTLAFEMSLVAFALMGNALVILAFVVDKNLRHRSYFFELNLAISDFV 64
QY 64 GAIAIPLYPSSLTFTWTSKQACVFWLITDYLLCTASVYNIYLISYDRQSVSNVWYRA 123
DB 65 GVISLPLYPHILFEMDPGKEICVFWLITDYLLCTASVYNIYLISYDRQSVSNVWYRA 124
QY 124 QHSGTWKATQWVAWVIFSEFMTNGPMILISDSWQNSTECCBPGFKWYFALPTSLLEFL 183
DB 125 QHTGVLLKIVTLVAVAVWVLAFLVNGPMILVSESWKDEGCEGFPSEWYLLAITSFLEFV 184
QY 184 IPLIVAFSAHIYWSLWKREKLSRCLSHPVLPSSSSSDHSGCRQDPSATLPARKE 243
DB 185 IPVILVAFNMNIYWSLWKRDHLSCQHPGLTA-VSSNICGHSFGRSLSRSLASST 243
QY 244 TTASIGSDKSRKSSLLPSIRAYKSNVNIASMGFLSHSDSLALQOREHIELEFRARLAK 303
DB 244 VPASFHSERQRRKSSLMFSRRTKMSNTIASMGFSQSDSVALHOREHVELLRARLAK 303
QY 304 SLAIIILAFALCMAVYSLTFTVYISFPPERNLTKSTWHTAFWLQWPNSEFVNPFLYPLCHK 363
DB 304 SLAIIILGFVAVCMVAYSLFTIVLSFYSSATGPKSVYRIAFWLQWPNSEFVNPFLYPLCHK 363
QY 364 RFQKAFKLILPVROSTP-PHNRIST 389
DB 364 RFQKAFKLIFCIKKOPLPSQHSRSVSS 390

RESULT 11
US-10-225-567A-629
; Sequence 629, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 629
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-225-567A-629

Query Match      64.3%; Score 1308.5; DB 14; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTALT-SIKSLTFELMSLAIATMLGNVVITAFIYDRNRHRSNFFELNLAIDPFV 63
DB 5 NSTILSLSTRVTTLAFEMSLVAFALMGNALVILAFVVDKNLRHRSYFFELNLAISDFV 64
QY 64 GAIAIPLYPSSLTFTWTSKQACVFWLITDYLLCTASVYNIYLISYDRQSVSNVWYRA 123
DB 65 GVISLPLYPHILFEMDPGKEICVFWLITDYLLCTASVYNIYLISYDRQSVSNVWYRA 124
QY 124 QHSGTWKATQWVAWVIFSEFMTNGPMILISDSWQNSTECCBPGFKWYFALPTSLLEFL 183
DB 125 QHTGVLLKIVTLVAVAVWVLAFLVNGPMILVSESWKDEGCEGFPSEWYLLAITSFLEFV 184
QY 184 IPLIVAFSAHIYWSLWKREKLSRCLSHPVLPSSSSSDHSGCRQDPSATLPARKE 243
DB 185 IPVILVAFNMNIYWSLWKRDHLSCQHPGLTA-VSSNICGHSFGRSLSRSLASST 243
QY 244 TTASIGSDKSRKSSLLPSIRAYKSNVNIASMGFLSHSDSLALQOREHIELEFRARLAK 303
DB 244 VPASFHSERQRRKSSLMFSRRTKMSNTIASMGFSQSDSVALHOREHVELLRARLAK 303
QY 304 SLAIIILAFALCMAVYSLTFTVYISFPPERNLTKSTWHTAFWLQWPNSEFVNPFLYPLCHK 363
DB 304 SLAIIILGFVAVCMVAYSLFTIVLSFYSSATGPKSVYRIAFWLQWPNSEFVNPFLYPLCHK 363
QY 364 RFQKAFKLILPVROSTP-PHNRIST 389
DB 364 RFQKAFKLIFCIKKOPLPSQHSRSVSS 390

RESULT 12
US-10-272-983-14
; Sequence 14, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Huang T.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-272-983-14

Query Match 64.3%; Score 1308.5; DB 14; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY NSTIATL-SIKISLTFLMSLAIATIMLGNVAVVLAFLVDRNLHRNSYFPLNLAIDPFV 63
DB NSTINLSLSTRVLAFLFMSLVAFAMLGNALVLAFLVDRNLHRNSYFPLNLAIDPFV 64
QY GAIAPLYIPSSLTWTSGKACVFWLITDYLLCTASVNNIVLISYDRYOSVNAWYRA 123
DB GAVISILYIPHTLFEBDFGKEICVFWLITDYLLCTASVNNIVLISYDRYOSVNAWYRA 124
QY QHSGTWKIAITOMVAVVIFSPMTNGPMILISDSQNSSTTECEPGFLKKYFALPTSLEFL 183
DB QHTGVAKIYTLMAVAVVLAFLVNGPMILVSESWKDSCEPFGFSEWYLAITSFLEFV 184
QY IPIILVAFSAHYMSLWMLREKLSRCLSHPLVPSDSSSDHGHSCQDPDRATLPARKE 243
DB IPIILVAFPMNMYMSLMKRDHLSCQSHPLTA-VSSNCGHSFGRULSSRSLASTE 243
QY TTASLSDSKSRKSSLLPSIRAYKSNVIAKMGFLSHSDSLAQQREHIEFPARKLAK 303
DB VPASFSEQRKSSLMPSRTMGNSNTIASKMGFSQSDSVALLHQREHIELARLAK 303
QY SLAILLAFAICAPYSLTIVISFPERNLTKSTYHTAFWLOMNSFVNPLYPYLCHK 363
DB SLAILGVFAVCAPYSLFTIVISFYSSATGPKSVYRIAFWLOMNSFVNPLYPYLCHK 363
QY RFOKAFKLIPVROSTP--PHNSIST 389
DB RFOKAFKLIFCIKQPLPSQHSRVS 390

RESULT 13

US-10-354-769-2
Sequence 2, Application US/10354769
Publication No. US20030149242A1
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: O'Reilly, Mark A.
APPLICANT: Peter, Beate
TITLE OF INVENTION: NOVEL POLYPEPTIDE
FILE REFERENCE: PCT0373B
CURRENT APPLICATION NUMBER: US/10/354,769
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 09/698,801
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/211,243
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: GB 9925641.4
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: GB 0009973.9
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-354-769-2

Query Match 64.3%; Score 1308.5; DB 14; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY NSTIATL-SIKISLTFLMSLAIATIMLGNVAVVLAFLVDRNLHRNSYFPLNLAIDPFV 63
DB NSTINLSLSTRVLAFLFMSLVAFAMLGNALVLAFLVDRNLHRNSYFPLNLAIDPFV 64

QY GAIAPLYIPSSLTWTSGKACVFWLITDYLLCTASVNNIVLISYDRYOSVNAWYRA 123
DB GAVISILYIPHTLFEBDFGKEICVFWLITDYLLCTASVNNIVLISYDRYOSVNAWYRA 124
QY QHSGTWKIAITOMVAVVIFSPMTNGPMILISDSQNSSTTECEPGFLKKYFALPTSLEFL 183
DB QHTGVAKIYTLMAVAVVLAFLVNGPMILVSESWKDSCEPFGFSEWYLAITSFLEFV 184
QY IPIILVAFSAHYMSLWMLREKLSRCLSHPLVPSDSSSDHGHSCQDPDRATLPARKE 243
DB IPIILVAFPMNMYMSLMKRDHLSCQSHPLTA-VSSNCGHSFGRULSSRSLASTE 243
QY TTASLSDSKSRKSSLLPSIRAYKSNVIAKMGFLSHSDSLAQQREHIEFPARKLAK 303
DB VPASFSEQRKSSLMPSRTMGNSNTIASKMGFSQSDSVALLHQREHIELARLAK 303
QY SLAILLAFAICAPYSLTIVISFPERNLTKSTYHTAFWLOMNSFVNPLYPYLCHK 363
DB SLAILGVFAVCAPYSLFTIVISFYSSATGPKSVYRIAFWLOMNSFVNPLYPYLCHK 363
QY RFOKAFKLIPVROSTP--PHNSIST 389
DB RFOKAFKLIFCIKQPLPSQHSRVS 390

RESULT 14

US-10-393-807-14
Sequence 14, Application US/10393807
Publication No. US20030175891A1
GENERAL INFORMATION:
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-tin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/10/393,807
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-393-807-14

Query Match 64.3%; Score 1308.5; DB 14; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY NSTIATL-SIKISLTFLMSLAIATIMLGNVAVVLAFLVDRNLHRNSYFPLNLAIDPFV 63
DB NSTINLSLSTRVLAFLFMSLVAFAMLGNALVLAFLVDRNLHRNSYFPLNLAIDPFV 64

DB 5 NSTILSLSTRVTLAFNMSLVAFAIMLGNALVILAFVVDKNLRHRSYFFLNLAISDFEV 64
QY 64 GAIAIPLYIPSSLYWTSKQACVFWLITDYLCTASVYNIIVLISYDRYQSVNNAWYRA 123
DB 65 GVISIPLYIPHLFEMDEGKEICVFWLITDYLCTASVYNIIVLISYDRYQSVNNAWYRA 124
QY 124 OHSGTWKATQWVAWVAFSFMNGPMILISDSWONSTTECEPGLKMYFALPTSLEFL 183
DB 125 QHTGVLTITLWVAWVLAFLVNGPMIIVSESWKDEGSECEPGEFSEWYILATISFLEFV 184
QY 184 IPILVAFSAHIYWSLWKREKLSRCLSHPVLPDSSSSDHSGSCROPPDSRATLPARKE 243
DB 185 IPVILVAFNMNIYWSLWKRDHLSCQSHPLGLTA-VSSNICGHSFRGRLSRSLASTE 243
QY 244 TTASIGSDKSRKSSSLPSIRAYKSNVYASMGFLSHSDSLALQOREHIELEFRAKRLAK 303
DB 244 VPASHSERQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRARRLAK 303
QY 304 SLAIIILAFATCWAPYSLTVTYISFPEERNLTGSTWYHTAFWLQWPNFVNPELYPLCHK 363
DB 304 SLAIIILGVFAVCWAPYSLTFTIVLSFYSSATGPKSVWYRIAFWLQWPNFVNPELYPLCHK 363
QY 364 RFQKAFKLIFCIKQPLPSQHSRSVSS 390
DB 364 RFQKAFKLIFCIKQPLPSQHSRSVSS 390

RESULT 15

US-10-417-820A-14

/ Sequence 14, Application US/10417820A
/ Publication No. US20030229216A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Liao, Chen W.
/ APPLICANT: Lowitz, Kevin
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Behan, Dominic P.
/ TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
/ FILE REFERENCE: 7.US28.CON
/ CURRENT APPLICATION NUMBER: US/10/417,820A
/ PRIOR APPLICATION NUMBER: 09/416,760
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: 60/110,060
/ PRIOR FILING DATE: 1998-11-27
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,852
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/123,944
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,945
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,948
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,951
/ PRIOR FILING DATE: 1999-03-12
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 155
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO. 14
/ LENGTH: 390
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-417-820A-14

Query Match 64.3%; Score 1308.5; DB 15; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106;

Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;
QY 5 NSTIALT-SIKISLTFNLSLAIAIMLGNVVIILAFIVDRNLRHRSNYFFLNLAISDFEV 63
DB 5 NSTILSLSTRVTLAFNMSLVAFAIMLGNALVILAFVVDKNLRHRSYFFLNLAISDFEV 64
QY 64 GAIAIPLYIPSSLYWTSKQACVFWLITDYLCTASVYNIIVLISYDRYQSVNNAWYRA 123
DB 65 GVISIPLYIPHLFEMDEGKEICVFWLITDYLCTASVYNIIVLISYDRYQSVNNAWYRA 124
QY 124 OHSGTWKATQWVAWVAFSFMNGPMILISDSWONSTTECEPGLKMYFALPTSLEFL 183
DB 125 QHTGVLTITLWVAWVLAFLVNGPMIIVSESWKDEGSECEPGEFSEWYILATISFLEFV 184
QY 184 IPILVAFSAHIYWSLWKREKLSRCLSHPVLPDSSSSDHSGSCROPPDSRATLPARKE 243
DB 185 IPVILVAFNMNIYWSLWKRDHLSCQSHPLGLTA-VSSNICGHSFRGRLSRSLASTE 243
QY 244 TTASIGSDKSRKSSSLPSIRAYKSNVYASMGFLSHSDSLALQOREHIELEFRAKRLAK 303
DB 244 VPASHSERQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRARRLAK 303
QY 304 SLAIIILAFATCWAPYSLTVTYISFPEERNLTGSTWYHTAFWLQWPNFVNPELYPLCHK 363
DB 304 SLAIIILGVFAVCWAPYSLTFTIVLSFYSSATGPKSVWYRIAFWLQWPNFVNPELYPLCHK 363
QY 364 RFQKAFKLIFCIKQPLPSQHSRSVSS 390
DB 364 RFQKAFKLIFCIKQPLPSQHSRSVSS 390

Search completed: August 3, 2005, 02:00:31
Job time: 160 secs

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OM protein - protein search, using sw model

Run on: August 3, 2005, 01:42:02 ; Search time 165 Seconds
(without alignments)
911.817 Million cell updates/sec

Title: US-10-626-398-10

Perfect score: 2036
Sequence: 1 MAA NSTALTSIKISLTL.....LKILPVROSTPPHNSISR 389

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1980s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2025	99.5	389	5	AAM50567
2	1308.5	64.3	390	3	AAB02831
3	1308.5	64.3	390	3	AAV71297
4	1308.5	64.3	390	4	AAB62445
5	1308.5	64.3	390	4	AAG64477
6	1308.5	64.3	390	4	AAB73622
7	1308.5	64.3	390	5	AAM53050
8	1308.5	64.3	390	5	ABP98629
9	1308.5	64.3	390	5	ABP78276
10	1308.5	64.3	390	5	AAM50564
11	1308.5	64.3	390	5	AAG66023
12	1308.5	64.3	390	5	AAU74906
13	1308.5	64.3	390	6	ABG71960
14	1308.5	64.3	390	6	ABU92265
15	1308.5	64.3	390	6	ABP81727
16	1308.5	64.3	390	6	AAE36417
17	1308.5	64.3	390	7	ADG98760
18	1308.5	64.3	390	7	ADJ26923
19	1308.5	64.3	390	8	ADG86375
20	1308.5	64.3	390	8	ADJ88376
21	1308.5	64.3	390	8	ADO05720
22	1308.5	64.3	390	8	ADO29496
23	1308.5	64.3	390	8	ADP20168
24	1308.5	64.3	390	8	ADQ75074
25	1308.5	64.3	391	5	AAM53052

26	1308.5	64.3	392	5	AAM53053
27	1306.5	64.2	390	4	AAM51410
28	1306.5	64.2	390	4	AAE36416
29	1303.5	64.0	390	8	ADG86522
30	1244	61.1	391	5	AAM50565
31	1244	61.1	391	8	ADO29497
32	1235.5	60.7	391	5	AAM50566
33	1166	57.3	357	6	AAB36415
34	1048.5	51.5	336	6	AAE36414
35	694.5	34.1	413	2	AAV22207
36	694.5	34.1	413	3	AAE15383
37	689.5	33.9	445	2	AAW92975
38	689.5	33.9	445	2	AAV06322
39	689.5	33.9	445	2	AAV67830
40	689.5	33.9	445	3	AAV92218
41	689.5	33.9	445	4	AAE30627
42	689.5	33.9	445	5	ABP79792
43	689.5	33.9	445	6	ABR43667
44	689.5	33.9	445	6	ABP57425
45	689.5	33.9	445	6	AAO19746

ALIGNMENTS

RESULT 1	
AA050567	AA050567 standard; protein; 389 AA.
AC	AA050567;
DT	18-MAR-2002 (first entry)
XX	Guinea pig histamine H4 receptor.
DE	Guinea pig histamine H4 receptor.
XX	Histamine H4 receptor; guinea pig; antiasmatic; antiallergenic;
KW	antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW	diagnosis; gene therapy.
XX	
OS	Cavia porcellus.
PN	WO200192485-A1.
XX	
PD	06-DEC-2001.
XX	
PF	22-FEB-2001; 2001MO-US005914.
XX	
PR	31-MAY-2000; 2000US-0208260P.
PA	(ORTH) ORTHO-MCNEIL PHARM INC.
XX	
PI	Lovenberg T, Liu C;
XX	
DR	WPI; 2002-114339/15.
DR	N-PSDB; AAT0983.
XX	
PT	New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT	the proteins; useful in gene therapy for treating diseases where it is
PT	beneficial to elevate mammalian histamine H4 receptor activity.
PS	Claim 13; Fig 6C; 92pp; English.
XX	
CC	The present sequence is that of a guinea pig histamine receptor of the H4
CC	subtype, as predicted from a cDNA clone isolated from a bone marrow
CC	library. The invention provides mammalian (human, mouse, rat and guinea
CC	pig) histamine H4 receptor nucleic acid molecules (see AAT0980-83) and
CC	polypeptides (see AAM50564-67). The nucleic acids have been expressed in
CC	recombinant host cells that produce active recombinant protein. The
CC	pharmacology of known histamine ligands is demonstrated. Mammalian
CC	histamine H4 receptor may be used in gene therapy for the treatment of
CC	diseases where it is beneficial to elevate mammalian histamine H4
CC	receptor activity. Recombinant protein is useful for identifying
CC	modulators of the histamine H4 receptor. Such modulators may be useful

CC for diagnosing, treating or preventing asthma, allergy, inflammation,
 CC cardiovascular and cerebrovascular disorders, non-insulin dependent
 CC diabetes mellitus, hypoglycemia, constipation, arrhythmia, disorders of
 CC the neuroendocrine system, stress and spasticity

XX Sequence 389 AA;

Query Match 99.5%; Score 2025; DB 5; Length 389;
 Best Local Similarity 99.7%; Pred. No. 8e-204;
 Matches 388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MANNSTLTSLTSLTFLMSLALAIAMGNVVVILAFIVDRNLHRNSYFFLMAIAD 60
 DB 1 MANNSTLTSLTSLTFLMSLALAIAMGNVVVILAFIVDRNLHRNSYFFLMAIAD 60
 QY 61 FVGAIAIPLVYIPSSLTWTSGKQACVFWLITDYLTCTASVYNIIVISYDRQVSNMAV 120
 DB 61 FVGAIAIPLVYIPSSLTWTSGKQACVFWLITDYLTCTASVYNIIVISYDRQVSNMAV 120
 QY 121 YPAQSGTWKIAITQWVAWVIFSMFNGPMILISDSQNSSTCEPGLKKWYFALPTSL 180
 DB 121 YPAQSGTWKIAITQWVAWVIFSMFNGPMILISDSQNSSTCEPGLKKWYFALPTSL 180
 QY 181 EFLIPIILVAVYSAHIYSLMKREKLSRCLSHPVLPDSSSDHGHSCRODPSRATLPA 240
 DB 181 EFLIPIILVAVYSAHIYSLMKREKLSRCLSHPVLPDSSSDHGHSCRODPSRATLPA 240
 QY 241 RKETTASIGSDSKSRKSSLPSTIRAYKNSNVIAASKGFLSHSDSLAQOREHIELFRARK 300
 DB 241 RKETTASIGSDSKSRKSSLPSTIRAYKNSNVIAASKGFLSHSDSLAQOREHIELFRARK 300
 QY 301 LAKSLAILLAFAICWAPYSLTTVIYSPFERNLTKSTWYHTAFWLQWNSFVNPLVPL 360
 DB 301 LAKSLAILLAFAICWAPYSLTTVIYSPFERNLTKSTWYHTAFWLQWNSFVNPLVPL 360
 QY 361 CHKRFQAKFLKILPVRRQSTPPHNRISIT 389
 DB 361 CHKRFQAKFLKILPVRRQSTPPHNRISIT 389

RESULT 2

AA02831 ID AAB02831 standard; protein; 390 AA.

XX AAB02831;
 AC
 XX
 DT 22-AUG-2000 (first entry)
 XX
 DE Human G protein coupled receptor hRUP7 protein SEQ ID NO:14.
 XX
 KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
 XX identification; agonist; screening; therapeutic; pharmaceutical; mutant.
 OS Homo sapiens.
 XX
 PN WO200022131-A2.
 PD 20-APR-2000.
 XX
 PF 13-OCT-1999; 99WO-US024065.
 XX
 PR 13-OCT-1998; 98US-00170496.
 PR 12-NOV-1998; 98US-0108029P.
 PR 20-NOV-1998; 98US-0109213P.
 PR 27-NOV-1998; 98US-0110060P.
 PR 16-FEB-1999; 99US-0120416P.
 PR 26-FEB-1999; 99US-0121852P.
 PR 12-MAR-1999; 99US-0123944P.
 PR 12-MAR-1999; 99US-0123945P.
 PR 12-MAR-1999; 99US-0123946P.
 PR 12-MAR-1999; 99US-0123948P.
 PR 12-MAR-1999; 99US-0123949P.
 PR 12-MAR-1999; 99US-0123951P.

PR 28-MAY-1999; 99US-0136436P.
 PR 28-MAY-1999; 99US-0136437P.
 PR 28-MAY-1999; 99US-0136439P.
 PR 28-MAY-1999; 99US-0137127P.
 PR 28-MAY-1999; 99US-0137131P.
 PR 28-MAY-1999; 99US-0137567P.
 PR 29-JUN-1999; 99US-0141448P.
 PR 27-AUG-1999; 99US-0151114P.
 PR 03-SEP-1999; 99US-0152524P.
 PR 29-SEP-1999; 99US-0156555P.
 PR 29-SEP-1999; 99US-0156633P.
 PR 29-SEP-1999; 99US-0156634P.
 PR 29-SEP-1999; 99US-0156653P.
 PR 01-OCT-1999; 99US-0157280P.
 PR 01-OCT-1999; 99US-0157281P.
 PR 01-OCT-1999; 99US-0157282P.
 PR 01-OCT-1999; 99US-0157294P.
 PR 01-OCT-1999; 99US-0157294P.
 PR 12-OCT-1999; 99US-00416760.
 PR 12-OCT-1999; 99US-00417044.
 XX
 PA (AREN-) ARENA PHARM INC.

XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
 PI Gore M, Hlaw CW, Lin I, Lowitz K, White C;
 XX
 DR WPI: 2000-317986/27.
 XX N-PSDB; AAA46023.

PT Non-endogenous, human G protein-coupled receptors for screening receptor,
 PT Inverse or partial agonists useful as therapeutic agents.

Example 1; Page 89-90; 187pp; English.

CC The present invention describes transmembrane receptors, preferably human
 CC G protein coupled receptors (GPCR), for which the endogenous ligand is
 CC unknown (orphan GPCR receptors). More specifically the present invention
 CC relates to non-endogenous, constitutively activated versions of a human
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct
 CC identification of candidate compounds as receptors agonists, inverse
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
 CC exemplification of the present invention

XX Sequence 390 AA;

Query Match 64.3%; Score 1308.5; DB 3; Length 390;
 Best Local Similarity 65.1%; Pred. No. 1.9e-128;
 Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRNSYFFLMAIADFV 63
 DB 5 NSTIALT-SIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRNSYFFLMAIADFV 63
 QY 64 GAIAPLYIPSSLTWTSGKQACVFWLITDYLTCTASVYNIIVISYDRQVSNMAVYRA 123
 DB 64 GAIAPLYIPSSLTWTSGKQACVFWLITDYLTCTASVYNIIVISYDRQVSNMAVYRA 123
 QY 65 GVISIPLYIPHTLFEWDRGKEICVFWLITDYLTCTASVYNIIVISYDRQVSNMAVYRT 124
 DB 65 GVISIPLYIPHTLFEWDRGKEICVFWLITDYLTCTASVYNIIVISYDRQVSNMAVYRT 124
 QY 124 QHSGTWKIAITQWVAWVIFSMFNGPMILISDSQNSSTCEPGLKKWYFALPTSLLEPL 183
 DB 124 QHSGTWKIAITQWVAWVIFSMFNGPMILISDSQNSSTCEPGLKKWYFALPTSLLEPL 183
 QY 184 IPIILVAVYSAHIYSLMKREKLSRCLSHPVLPDSSSDHGHSCRODPSRATLPAKRE 243
 DB 184 IPIILVAVYSAHIYSLMKREKLSRCLSHPVLPDSSSDHGHSCRODPSRATLPAKRE 243
 QY 244 TTAASIGSDSKSRKSSLPSTIRAYKNSNVIAASKGFLSHSDSLAQOREHIELFRARK 303
 DB 244 TTAASIGSDSKSRKSSLPSTIRAYKNSNVIAASKGFLSHSDSLAQOREHIELFRARK 303
 QY 304 SLAIIILAFALCWAAPYSLTTVIYSPFERNLTKSTWYHTAFWLQWNSFVNPLVPLCHK 363
 DB 304 SLAIIILAFALCWAAPYSLTTVIYSPFERNLTKSTWYHTAFWLQWNSFVNPLVPLCHK 363

XX New G-protein coupled receptor-like polypeptide, polynucleotide for
PT screening drug candidates for treating diseases associated with signal
PT transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
XX
XX Claim 22; Page 44; 66pp; English.

XX This is a human G-protein coupled receptor (GPCR)-like polypeptide, PFI-
CC 013, encoded by cDNA of NCIMB 41073. The PFI-013 protein can be expressed
CC by standard recombinant methodology. Antibodies and modulators of PFI-013
CC are useful in the manufacture of a medicament for treating allergic
CC disorder, including extrinsic asthma, immunological disorders, such as
CC intrinsic asthma, vasculitic granulomatous disease, interstitial and
CC other pulmonary disease, including chronic obstructive pulmonary disease
CC (COPD), infectious, inflammatory disease, such as inflammatory bowel
CC disease and neoplastic and myeloproliferative diseases. They are also
CC useful for treating obesity, diabetes, metabolic, neurological diseases,
CC psychotherapeutics, urogenital disease, reproduction and sexual medicine,
CC inflammation, cancer, tissue repair, dermatology, photocaging, skin
CC pigmentation, osteoporosis, cardiovascular, gastrointestinal diseases,
CC allergy and respiratory disease, sensory organ disorders, sleep disorders
CC and hair loss. The PFI-013 protein and nucleic acid are useful in the
CC diagnosis and treatment of the above conditions and also for screening
CC drug candidates for the treatment of diseases associated with signal
CC transduction. The antibodies are also useful for enrichment of
CC eosinophils from mammalian, especially human blood and for detecting the
CC protein in biological samples
XX

XX Sequence 390 AA:

Query Match 64.3%; Score 1308.5; DB 4; Length 390;
Best Local Similarity 65.1%; Pred. No. 1.9e-128;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTILALT-SIKISLTFELMSLAIAIMLGNVVVILAFIVDRNIRHRSNYFFLNLAIADFFV 63
DB 5 NSTILSLSTRVTTLAFPMSLVAFALMGNALVILAFVVDKLNRRSSYFFLNLAIADFFV 64
QY 64 GAIAIPLVPSLSLTWTSGKQACVFWLITDYLLCTASVNIYLISYDRQSVSNVWYRA 123
DB 65 GVISIPLYIPIHTLFEMDEGKEICVFWLITDYLLCTASVNIYLISYDRQSVSNVWYRT 124
QY 124 QHSGTWKATQWVAWVIFSFMTNGPMILISDSWQNSTECEPGLKKYFALPTSLLEFL 183
DB 125 QHTGVLTITVLMVAWVLAFLVNGPMILVSESKDEGSECEGFESEWYIILAITSEFLERV 184
QY 184 IPIILVAVSAHIYWSLWKREKLSRCLSHPVLPSSDSSSDHSGCRDPDSRATLPARKE 243
DB 185 IPVILVAFNNMIYWSLWKRDHLRSQSHPGULTA-VSSNICGHSFGRSLSRSSASTE 243
QY 244 TTASISGDSKSRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLALOOREHIELFRARKLAK 303
DB 244 VPASHSERQRKSSLMFSRRTKMSNTIASKMGFSQSDSVALHQREVELLRARRLAK 303
QY 304 SLAIIILGFAVCMAPYSLTFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLVPLCHK 363
DB 304 SLAIIILGFAVCMAPYSLTFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLVPLCHK 363
QY 364 RFQKAFKLKIPVRROSTP-PHNRST 389
DB 364 RFQKAFKLKIPVRROSTP-PHNRST 389

RESULT 5
AAG64477
ID AAG64477 standard; protein; 390 AA.

XX AAG64477;
XX
XX 25-SEP-2001 (first entry)
XX
XX Human G protein-coupled receptor protein BG26.
XX

KW Human; G protein-coupled receptor protein BG26; histamine H3; histamine;
KW altering intracellular cAMP concentration;
KW regulating signal transduction.

XX Homo sapiens.

XX WO200146414-A1.

XX 28-JUN-2001.

XX 20-DEC-2000; 2000WO-JP009038.

XX 20-DEC-1999; 99JP-00361687.

XX (BANY) BANYU PHARM CO LTD.

XX Itadant H, Nakamura T, Tanaka K, Ohta M;

XX WPI; 2001-441675/47.

XX N-PSDB; AAH47911.

PT G protein-coupled receptor protein BG26, with activity of binding to
PT histamine and capable of changing intracellular cAMP concentration in
PT response to its stimulus, applicable as tool in screening ligands or drug
PT candidates.

PS Claim 1; Page 41-44; 50pp; Japanese.

CC The present sequence is that of the human G protein-coupled receptor
CC protein BG26, which shows significant homology with histamine H3, with
CC activity of binding to histamine and capable of changing intracellular
CC cAMP concentration in response to its stimulus. The protein is applicable
CC as a tool in screening ligands or drug candidates for regulating signal
CC transduction from such protein and treating diseases associated with its
CC abnormality
XX

XX Sequence 390 AA:

Query Match 64.3%; Score 1308.5; DB 4; Length 390;
Best Local Similarity 65.1%; Pred. No. 1.9e-128;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTILALT-SIKISLTFELMSLAIAIMLGNVVVILAFIVDRNIRHRSNYFFLNLAIADFFV 63
DB 5 NSTILSLSTRVTTLAFPMSLVAFALMGNALVILAFVVDKLNRRSSYFFLNLAIADFFV 64
QY 64 GAIAIPLVPSLSLTWTSGKQACVFWLITDYLLCTASVNIYLISYDRQSVSNVWYRA 123
DB 65 GVISIPLYIPIHTLFEMDEGKEICVFWLITDYLLCTASVNIYLISYDRQSVSNVWYRT 124
QY 124 QHSGTWKATQWVAWVIFSFMTNGPMILISDSWQNSTECEPGLKKYFALPTSLLEFL 183
DB 125 QHTGVLTITVLMVAWVLAFLVNGPMILVSESKDEGSECEGFESEWYIILAITSEFLERV 184
QY 184 IPIILVAVSAHIYWSLWKREKLSRCLSHPVLPSSDSSSDHSGCRDPDSRATLPARKE 243
DB 185 IPVILVAFNNMIYWSLWKRDHLRSQSHPGULTA-VSSNICGHSFGRSLSRSSASTE 243
QY 244 TTASISGDSKSRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLALOOREHIELFRARKLAK 303
DB 244 VPASHSERQRKSSLMFSRRTKMSNTIASKMGFSQSDSVALHQREVELLRARRLAK 303
QY 304 SLAIIILGFAVCMAPYSLTFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLVPLCHK 363
DB 304 SLAIIILGFAVCMAPYSLTFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLVPLCHK 363
QY 364 RFQKAFKLKIPVRROSTP-PHNRST 389
DB 364 RFQKAFKLKIPVRROSTP-PHNRST 389

RESULT 6
AAB73622

ID AAB73622 standard; protein: 390 AA.
 AC AAB73622:
 DT 10-AUG-2001 (first entry)
 DE Human G protein-coupled receptor AXOR35.
 KM AXOR35; human; G protein-coupled receptor; 7TM receptor;
 KM histamine H3 receptor homologue; infection; viral; bacterial; fungal;
 KM protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
 KM bulimia; osteoporosis; asthma; allergy; urinary retention;
 KM acute heart failure; hypotension; hypertension; angina pectoris;
 KM myocardial infarction; stroke; ulcer; migraine; vomiting;
 KM psychotic disorder; neurological disorder; anxiety; schizophrenia;
 KM manic depression; bipolar disorder; depression; delirium; dementia;
 KM severe mental retardation; dyskinesia; Parkinson's disease;
 KM Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;
 KM macrophage; eosinophil; neutrophil; function modulation;
 KM autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
 KM drug screening; signal transduction; transgenic animal; drug discovery.
 OS Homo sapiens.
 XX MO200133221-A1.
 XX 10-MAY-2001.
 XX 26-OCT-2000; 2000WO-US029461.
 PF 02-NOV-1999; 99US-00431898.
 PR 03-FEB-2000; 2000US-00497790.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI (SMIK) SMITHKLINE BEECHAM PLC.
 PA Aubart KM, Bergama DJ, Fitzgerald LR, Graybill TL, Li X;
 PI Michalovich D, Morrow DM, Zhu Y;
 DR N-PSDB; AAH24007.
 DR WPI; 2001-316464/33.
 PT Novel G-protein coupled receptor polypeptide and polynucleotide for
 PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological
 PT disorders and for identifying modulators useful for treating asthma.
 PS Claim 1; Page 50-51; 54pp; English.
 XX The invention relates to the human G protein-coupled receptor AXOR35
 CC (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments
 CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative
 CC transmembrane domains and is involved in signal transduction. AXOR35 has
 CC homology and structural similarity with G protein-coupled receptors such
 CC as the human histamine H3 receptor. The invention also relates to
 CC expression vectors and host cells comprising AXOR35 DNA, to recombinant
 CC expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins
 CC and nucleotides may be used to create a wide variety of disorders
 CC including bacterial, fungal, protozoal and viral infections, particularly
 CC HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy;
 CC diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;
 CC urinary retention; acute heart failure; hypotension; hypertension; angina
 CC pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;
 CC psychotic and neurological disorders such as anxiety, schizophrenia,
 CC manic depression, depression, delirium, dementia, and severe mental
 CC retardation, and dyskinesias, such as Parkinson's disease, Huntington's
 CC disease or Gilles de la Tourette's syndrome. AXOR35 proteins and
 CC nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and
 CC antibodies may be used in screening compounds for their ability to
 CC modulate AXOR35 activity or expression. Such AXOR35 modulators are
 CC particularly useful for treating asthma, and inhibiting or promoting the
 CC function of lymphocytes, macrophages, eosinophils or neutrophils in
 CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also
 CC useful for diagnosing or determining susceptibility of an individual to a

CC disease via the detection of abnormal levels of protein or mRNA, or via
 CC the detection of mutations in the corresponding gene. AXOR35 proteins are
 CC also useful for inducing an immunological response in a mammal against
 CC the above diseases, and for antibody production. AXOR35 nucleotides are
 CC also useful as diagnostic reagents, in chromosome localisation and tissue
 CC expression studies, and for producing transgenic animals useful in drug
 CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35
 CC protein or fragments thereof, and are also useful for treating conditions
 CC associated with the expression of the AXOR35 protein. The present
 CC sequence represents human AXOR35
 XX
 XX Sequence 390 AA:
 SQ
 Query Match 64.3%; Score 1308.5; DB 4; Length 390;
 Best Local Similarity 65.1%; Pred. No. 1,9e-128;
 Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;
 QY 5 NSTAIATL-SIKISLTPFLMSLAIAMLGNNVVIATFYDNLHRNSYFPLNIAIDFFV 63
 DB 5 NSTINSLSTRVTLAFPMFSLVAFALMGNALVITAFVDKNLHRSSYFPLNIAISDFV 64
 QY 64 GATAIPLYIPSSLTYYTSGQACVFWLIDYLLCTASVYNYVILISYDRYSVSNNAWYRA 123
 DB 65 GVISIPLYIPHTLFWDPGKEICVFWLITDYLLCTASVYNYVILISYDRYLSVSNAYSRT 124
 QY 124 QHSQTKIATOWAAVWIFSPMTNGPMILISDSQNSSTTECEPGFLKKWYFALPTSLLEFL 183
 DB 125 QHTGVLLKYITLMAVAVLAFVNGPMILVSESKMDECSBEPFSEWYLIATLSFLEFV 184
 QY 184 IPIILVAVPSAHITWYSLMKREKLSRCLSHFVLPSDSSSDHGSCHODPDPSRAATLPARKE 243
 DB 185 IPIILVAVFMNITWYSLMKRDLHSRCQSHGFLRA-VSSNICGSPGRLSSRSLSASTE 243
 QY 244 TTASLSGDSKRRKSSLLPSTRAYKSNVITASKKGFLSHSSSLAQREHLEPRARLAK 303
 DB 244 VPASFHSERORRKSLSMFSRTYNSNTIASKXGFSQSSVALHOREHELLRARRLAK 303
 QY 304 SLAIILAAPAICWAPSLTITVYSPFERNLTKSTWHTAFWLOWFSFVNPPLYPLCHK 363
 DB 304 SLAILGVPAVCAPSLTITVLSFYSSATGPSSWYRIAFWLOWNSFNPILYPLCHK 363
 QY 364 RFQKAFKLIPVRQSTP-PHNRISST 389
 DB 364 RFQKAFKLIPCIKKQPLPSQHSRSVSS 390
 RESULT 7
 ID AAM53050 standard; protein: 390 AA.
 XX AAM53050:
 XX 26-MAR-2002 (first entry)
 DE Human G protein-coupled receptor nGPCR-2067.
 KM Human; nGPCR-2067; G protein-coupled receptor; 7TM receptor;
 KM signal transduction; mental disorder; central nervous system disease;
 KM metabolic disease; infection; HIV-1; HIV-2; pain; neurological disorder;
 KM psychotic disorder; Huntington's disease; schizophrenia; migraine;
 KM depression; anxiety; bipolar disorder; dementia; Alzheimer's disease;
 KM Parkinson's disease; proliferative disorder; cancer; psoriasis;
 KM benign prostatic hypertrophy; diabetes; dyslipidemia; obesity; anorexia;
 KM thyroid disorder; cardiovascular disease; hypotension; hypertension;
 KM thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis;
 KM inflammatory conditions; autoimmune disorder; rheumatoid arthritis;
 KM hormonal disorder; renal failure; anti-HIV; analgesic; cytostatic;
 KM antidiabetic; metabolic; hypertensive; hypotensive; thrombolytic;
 KM cardiant; antithrombotic; neuroleptic; antimigraine;
 KM antiparkinsonian; tranquilizer; antidepressant; neuroprotective;
 KM anticonvulsant; antiinflammatory; antirheumatic; antiarthritic;
 KM antipsoriatic; gene therapy; receptor.

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain /label= Transmembrane_domain_1
FT Domain /label= Transmembrane_domain_2
FT Domain /label= Transmembrane_domain_3
FT Domain /label= Transmembrane_domain_4
FT Domain /label= Transmembrane_domain_5
FT Domain /label= Transmembrane_domain_6
FT Domain /label= Transmembrane_domain_7
FT Domain /label= Transmembrane_domain_7
FN WO200185793-A2.
PD 15-NOV-2001.
PR 08-MAY-2001; 2001WO-US014750.
PR 08-MAY-2000; 2000US-0203108P.
PA (PHEA) PHARMACIA & UPJOHN CO.
PI Lind P, Sejlitz T, Vogel G, Wood LS;
DR WPI; 2002-062240/08.
DR N-PSDB; ABA02496.
PT New polynucleotide, useful for identifying modulator compounds which are used for treating psoriasis, schizophrenia, diabetes, encodes the novel G protein-coupled receptor (nGPCR) polypeptide (nGPCR-2067).
PS Claim 31; Page 63; 100pp; English.
XX
XX This sequence represents a novel human G protein-coupled receptor (GPCR) designated nGPCR-2067. Like all GPCRs, nGPCR-2067 has 7 putative transmembrane domains and is involved in signal transduction. The invention also relates to expression vectors and host cells comprising nucleic acids encoding nGPCR-2067, to recombinant expression of nGPCR-2067, to antibodies specific for nGPCR-2067, to drug screening methods that use nGPCR-2067, and to modulators of nGPCR-2067 activity. nGPCR-2067 nucleic acid sequences may be used to isolate nGPCR-2067 allelic variants and species homologues and may also be used in genetic mapping. The invention also discloses the use of nGPCR-2067 nucleic acids in screening for a predisposition to nGPCR-2067-associated hereditary mental disorders, or for the diagnosis of these disorders. nGPCR-2067 nucleic acids may additionally be used to generate transgenic animals, including knockout animals, which may provide an insight into treating a variety of human disorders, and may also be used in the design of antisense molecules for suppressing expression of nGPCR-2067 in cells. nGPCR-2067, and nGPCR-2067 modulators may be used to treat a wide variety of medical conditions, particularly mental disorders, central nervous system diseases, and metabolic diseases. Diseases that may be treated include viral infections, particularly HIV-1 or HIV-2 infections; pain; central nervous system, neurological and psychotic disorders such as Huntington's disease, schizophrenia, migraine, depression, anxiety, bipolar disorder, dementia, Alzheimer's disease, and Parkinson's disease; proliferative disorders such as cancer, benign prostatic hypertrophy and psoriasis; metabolic disorders such as diabetes, dyslipidemia, obesity, and anorexia; thyroid disorders; cardiovascular diseases such as hypotension, hypertension, thrombosis, myocardial infarction, cardiomyopathies, and atherosclerosis; inflammatory conditions; autoimmune disorders (e.g., rheumatoid arthritis); hormonal disorders; and renal failure
XX
XX Sequence 390 AA;
Query Match 64.3%; Score 1308.5; DB 5; Length 390;
Best Local Similarity 65.1%; Pred. No. 1.9e-128;

Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;
OY 5 NSTIALT-SIKISLTFMSLLAIAIMLGNVVIIAFIDRNLRHSNFFNLAIADPFV 63
DB 5 NSTIULSISTRTVTLAFPMISLVAFAIMLGNALVITLAFVDKILRHSSYFFNLAIADPFV 64
OY 64 GAIALPLVIPSLLTYWTSKQACVFWLITDYLCTASYNYNIVLISYDRQVSNAWYRA 123
DB 65 GVISIPLYIPHTLFEMDFGKEICVFWLITDYLCTASYNYNIVLISYDRQVSNAVSYRT 124
OY 124 QHSGTWKATQWVAVMISFMTNGPMILISDSQWONSTECBCEGFLKRYFALPTSLLEFL 183
DB 125 QHTGVLKVTLMVAWVIALFVNGPMILIVSEWKGEGCEGFSEWTLAITSFLEFV 184
OY 184 IPIILVAFSAHYVSLWKREKLSRCLSPVLPDSSSDSHGSRQPDSPATYPARKE 243
DB 185 IPIVILVAFPMNVIYSLMKRDLHSRCQHPGLTA-VSSNICGHSRGRSLSRSSASTE 243
OY 244 TTASLGSDDRKSSLLPSIRAYKSNVIAASKGFLSHSDSLAQOREHIELFRARKLAK 303
DB 244 VPASFHSRQRKSSLSMFSSRTKNNSNTIASKGSFQSDSVLAHQREHIELFRARKLAK 303
OY 304 SLATILAFALCMAPYSLTTYIYSPFPRNLTKSTWYHTAFWLFQFNFPFLYPLCHK 363
DB 304 SLATILGVFAVCWAPYSLFTVLSFYSSATGPKSVYRIAFWLFQFNFPVNLPLCHK 363
OY 364 RFOKAFILKILPVROSTP-PHNSISIT 389
DB 364 RFOKAFILKILKQPLPSQHSRSYVS 390
RESULT 8
ABP98629
ID ABP98629 standard; protein; 390 AA.
XX
XX ABP98629;
XX
XX 13-JUN-2003 (first entry)
XX
XX Human histamine receptor SP9144.
DE
XX human; histamine receptor; chromosome 18; anti-inflammatory;
KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;
KW anti-migraine; cardiac; anti-rheumatic; anti-arthritis; antipsoriatic;
KW neuroprotective; inflammatory; asthma; allergy; atopic dermatitis;
KW myocardial infarction; migraine; chronic obstructive pulmonary disease;
KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
KW psoriasis; receptor.
XX
XX Homo sapiens.
OS
XX US6204017-B1.
PN
XX 20-MAR-2001.
XX
XX 07-OCT-1999; 99US-00414010.
XX
XX 07-OCT-1999; 99US-00414010.
PR
XX 07-OCT-1999; 99US-00414010.
XX
XX (SCHE) SCHERING CORP.
PA Behan JX, Hedrick JA, Laz TM, Monema FJ, Morse KL, Umland SP;
PI Wang S;
XX
XX WPI: 2002-442063/47.
DR N-PSDB; AB280663.
XX
XX New nucleic acid encoding antigenic part of human histamine receptor, useful for preparing antibodies, e.g. for treating-histamine related disorders.
PT
XX
XX Example 1; Col 27-30; 19pp; English.
PS
XX

This sequence represents the amino acid sequence of a human histamine receptor (HR) designated SP9144. The sequence was isolated by searching databases with the sequence of known G-coupled protein receptor (GPCR). The gene is used for recombinant production of HR and for preparing antibodies (Ab). These Ab are used to purify HR by immunoprecipitation chromatography. In immunoblotting of histamine receptor, to identify cDNA clones that express the receptor, as antagonist to block binding of histamine (for treating any histamine-associated disorder) and to generate anti-idiotypic antibodies. Agonists and antagonists of the HR protein can be used in the treatment of e.g. inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease, rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.

Sequence 390 AA:

Query Match 64.3%; Score 1308.5; DB 5; Length 390;
Best Local Similarity 65.1%; Pred. No. 1.9e-128;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY NSTIALT-SIKISLTFMLSLAIAIMLGNNVVLAFVVDNLRHRSNYFFLNIAIDFFV 63
DB NSTIINSLSTRVTLAFPMSLVAFALMGNALVILAFVVDNLRHRSNYFFLNIAIDFFV 64
QY GAIAIPLYIPSSLTWTSGKQACVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYWYRA 123
DB GVISITPLYIPHTLFEMDFGKEICVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYWYRA 124
QY 124 QHSGTWKATQWYAVVIFSPMTNGPMILISDSQNSTTECEPFLKKWYFALPTSLEFL 183
DB 125 QHTGVAKITVLWVAVVLAFLVNGPMILVSESWKDEGSECEPFSFEMWYLAITSFLEFV 184
QY 184 IPIILVAYSANHYWLSMKREKLSRCLSHPVLPSSDSSSDHSGSCODPDRAATLPARKE 243
DB 185 IPIILVAYSANHYWLSMKREKLSRCLSHPVLPSSDSSSDHSGSCODPDRAATLPARKE 243
QY 244 TTSALGSDKSRKSSLLPSIRAYKSNVIAKMGFLSHSDSLAQQREHTEFRARLAK 303
DB 244 VPASFHSERGRKSSLMFSRRTGNSNTIASKKGSGSOSVALHREHTEFRARLAK 303
QY 304 SLAIIILGAVFAVCWAPSLFTIVLSFYSSATGPKSVWYRIAFMLQWNSFVNPLYPPLCHK 363
DB 304 SLAIIILGAVFAVCWAPSLFTIVLSFYSSATGPKSVWYRIAFMLQWNSFVNPLYPPLCHK 363
QY 364 RFOKAFKILPVRRGSTR-PHNSISST 389
DB 364 RFOKAFKILPVRRGSTR-PHNSISST 389

RESULT 9

ABR78276 standard; protein; 390 AA.

AC ABR78276;

DT 05-DEC-2002 (first entry)

DE Amino acid sequence of human histamine receptor.

Human; histamine receptor; receptor; inflammation; asthma; allergy;
atopic dermatitis; stroke; myocardial infarction; migraine;
chronic obstructive pulmonary disease (COPD); rheumatoid arthritis;
multiple sclerosis; inflammatory bowel disease; psoriasis;
intracellular second messenger pathway; cellular growth rate;
hormone secretion.

OS Homo sapiens.

XX US2002098539-A1.

XX 25-JUL-2002.

XX 19-MAR-2001; 2001US-00812216.

XX 07-OCT-1999; 99US-00414010.

PA (BEHA/) BEHAN J X.
PA (HEDR/) HEDRICK J A.
PA (LAZT/) LAZ T M.
PA (MONS/) MONSMA F J.
PA (MORS/) MORSE K L.
PA (UMLA/) UMLAND S P.
PA (WANG/) WANG S.

PI Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP,
PI Wang S;

DR WPI: 2002-673827/72.

DR N-PSDB; ABR78739.

PT Novel mammalian histamine receptor polypeptide useful for identifying
agonist or antagonist for treating diseases such as inflammation, asthma,
stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.

PS Claim 2; Page 16-17; 21pp; English.

CC The present sequence represents a histamine receptor. The polypeptide is
CC useful for identifying an agonist or antagonist of a mammalian histamine
CC receptor. It is useful as an antigen to elicit the production of
CC antibodies. The histamine receptor polypeptide and polynucleotide are
CC useful in the treatment and management of diseases such as inflammation,
CC asthma, allergy, atopic dermatitis, stroke, myocardial infarction,
CC migraine, chronic obstructive pulmonary disease (COPD), rheumatoid
CC arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.
CC They are also useful for modulating intracellular second messenger
CC pathway activated through histamine receptors (cyclic-AMP, calcium,
CC inositol phosphate and mitogen activated protein (MAP) kinase), changes
CC in cellular growth rate, secretion of hormones, receptor-stimulated Ca²⁺
CC mobilization, mitogenic effects, etc

Sequence 390 AA:

Query Match 64.3%; Score 1308.5; DB 5; Length 390;
Best Local Similarity 65.1%; Pred. No. 1.9e-128;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFMLSLAIAIMLGNNVVLAFVVDNLRHRSNYFFLNIAIDFFV 63
DB 5 NSTIINSLSTRVTLAFPMSLVAFALMGNALVILAFVVDNLRHRSNYFFLNIAIDFFV 64
QY 64 GAIAIPLYIPSSLTWTSGKQACVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYWYRA 123
DB 65 GVISITPLYIPHTLFEMDFGKEICVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYWYRA 124
QY 124 QHSGTWKATQWYAVVIFSPMTNGPMILISDSQNSTTECEPFLKKWYFALPTSLEFL 183
DB 125 QHTGVAKITVLWVAVVLAFLVNGPMILVSESWKDEGSECEPFSFEMWYLAITSFLEFV 184
QY 184 IPIILVAYSANHYWLSMKREKLSRCLSHPVLPSSDSSSDHSGSCODPDRAATLPARKE 243
DB 185 IPIILVAYSANHYWLSMKREKLSRCLSHPVLPSSDSSSDHSGSCODPDRAATLPARKE 243
QY 244 TTSALGSDKSRKSSLLPSIRAYKSNVIAKMGFLSHSDSLAQQREHTEFRARLAK 303
DB 244 VPASFHSERGRKSSLMFSRRTGNSNTIASKKGSGSOSVALHREHTEFRARLAK 303
QY 304 SLAIIILGAVFAVCWAPSLFTIVLSFYSSATGPKSVWYRIAFMLQWNSFVNPLYPPLCHK 363
DB 304 SLAIIILGAVFAVCWAPSLFTIVLSFYSSATGPKSVWYRIAFMLQWNSFVNPLYPPLCHK 363
QY 364 RFOKAFKILPVRRGSTR-PHNSISST 389
DB 364 RFOKAFKILPVRRGSTR-PHNSISST 389

RESULT 10

AAM50564
 ID AAM50564 standard; protein; 390 AA.
 AC AAM50564;
 DT 18-MAR-2002 (first entry)
 DE Human histamine H4 receptor.
 XX
 XX Histamine H4 receptor; human; antiasmatic; antiallergenic;
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
 KM diagnosis; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO200192485-A1.
 XX
 XX 06-DEC-2001.
 XX
 XX 22-FEB-2001; 2001WO-US005914.
 XX
 XX 31-MAY-2000; 2000US-0208260P.
 XX
 XX (ORTH) ORTHO-MCNEIL PHARM INC.
 XX
 XX Lovenberg T, Liu C;
 XX
 XX WPI; 2002-114339/15.
 DR N-PSDB; AAI70980.
 XX
 XX
 PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
 PT the proteins, useful in gene therapy for treating diseases where it is
 PT beneficial to elevate mammalian histamine H4 receptor activity.
 XX
 PS Claim 13; Fig 2; 92pp; English.
 XX
 XX The present sequence is that of a human histamine receptor of the H4
 CC subtype, as predicted from a cDNA clone isolated from a bone marrow CDNA
 CC library. The invention provides mammalian (human, mouse, rat and guinea
 CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in
 CC recombinant host cells that produce active recombinant protein. The
 CC pharmacology of known histamine ligands is demonstrated. Mammalian
 CC histamine H4 receptor may be used in gene therapy for the treatment of
 CC diseases where it is beneficial to elevate mammalian histamine H4
 CC receptor activity. Recombinant protein is useful for identifying
 CC modulators of the human histamine H4 receptor. Such modulators may be
 CC useful for diagnosing, treating or preventing asthma, allergy,
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
 CC disorders of the neuroendocrine system, stress and spasticity
 CC
 SQ Sequence 390 AA;
 Query Match 64.3%; Score 1308.5; DB 5; Length 390;
 Best Local Similarity 65.1%; Pred. No. 1.9e-128;
 Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;
 QY 5 NSTILT-SIKSTIFELSLAIAIMLGWVVIATIVVRNLRHSNYFELALADPFV 63
 DB 5 NSTINLSLSTRVTLAFEMSLVAFALMGALVLAIVDKNRHSNYFELALADPFV 64
 QY 64 GAIAIPLYPSLSLWTSGKQACVFWLIDYLLCTASVNIIVLISYDRYQSVNAWVYA 123
 DB 65 GVISIFPLVPHLTFEIDPKKEICVFWLTDYLLCTASVNIIVLISYDRYQSVNAWVYA 124
 QY 124 QHSGTWKATQWAAVWIFSFMTNGPMILISDMQNSTTECEPGLKKWYFALPTSLLEFL 183
 DB 125 QHTGVAKITVTLWAAVWVLAFLVNGPMILVSESKDEGSECEPGEFSEWYLLAITSFLEFV 184
 QY 184 ILLIIVAFSAHIWYSLMKREKLSRCLSHPVLPSSDSSSDHSHSCQDDPSAATLPARE 243
 DB 185 IPIVILVAFNMNIWYSLMKRDLHLSRCQSHPGTLA-VSSNICGHSFGRSLSSRSLSASTE 243

QY 244 TTASIGSDKSRKSSILPSIRAYKNSNVIASKMGLSHSDSLALQOREHILFRAKRLAK 303
 DB 244 VPASFHSERQRRKSSILMFSNRTKMSNTIASMGSSFQSDSVLALHGREHVELLRARRLAK 303
 QY 304 SLATILAFALCMAPYSITTYIYSPFPERNLTKSWHTAFWLPQFNSTVNFPLPLCHK 363
 DB 304 SLATILGVFAVCMAPYSITTYIYSPFPERNLTKSWHTAFWLPQFNSTVNFPLPLCHK 363
 QY 364 RFQKAFILKLPVROSTP-PHNRISIST 389
 DB 364 RFQKAFILKLPVROSTP-PHNRISIST 390
 RESULT 11
 AAG66023
 ID AAG66023 standard; protein; 390 AA.
 XX
 XX AAG66023;
 XX
 XX 27-FEB-2002 (first entry)
 DT
 XX
 DE Human histamine H4 receptor protein.
 XX
 KW Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive;
 KW antiasmatic; antiallergic; neuroprotective; antidiabetic; human;
 KM cerebroprotective; CAMP modulator; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 12..40
 FT /note= "transmembrane domain"
 FT Domain 52..69
 FT /note= "transmembrane domain"
 FT Domain 88..110
 FT /note= "transmembrane domain"
 FT Domain 130..154
 FT /note= "transmembrane domain"
 FT Domain 172..196
 FT /note= "transmembrane domain"
 FT Domain 304..325
 FT /note= "transmembrane domain"
 FT Domain 342..362
 FT /note= "transmembrane domain"
 PN WO200185786-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 04-MAY-2001; 2001WO-US014527.
 XX
 XX 05-MAY-2000; 2000US-0202151P.
 PR 23-AUG-2000; 2000US-0227567P.
 PR 13-NOV-2000; 2000US-0247855P.
 XX
 XX (AMHP) AMERICAN HOME PROD CORP.
 XX
 PI Jones PG, Blatcher M, Wu S, Pausch MH;
 XX
 DR WPI; 2002-049442/06.
 DR N-PSDB; AAI67750.
 XX
 PT New histamine receptor, termed H4 useful for detecting H4 (ant)agonists
 PT for treating transplanted organ rejection, asthma, allergy, multiple
 PT sclerosis and rheumatoid arthritis.
 XX
 PS Claim 5; Fig 1; 66pp; English.
 CC The invention provides an isolated histamine receptor, H4, which binds
 CC ligands comprising imidazole attached to amine by an alkyl chain. The H4
 CC receptor can be expressed by standard recombinant methodology. Cells
 CC expressing H4 receptor protein at a detectable level can suppress cyclic

CC adenosine monophosphate (cAMP) formation when contacted with the H4
 CC receptor agonist. The H4 receptor and antibodies are used for identifying
 CC H4 receptor modulators. Modulation of histamine H4 receptors is useful
 CC for treating transplanted organ rejection, asthma, allergies and
 CC autoimmune pathologies such as multiple sclerosis, type I diabetes,
 CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor
 CC protein and nucleic acids are useful targets to identify drugs that are
 CC effective in treating disorders associated with histamine-regulated
 CC processes. Identification and isolation of H4 receptor provides for
 CC development of screening of molecules that interact with H4 receptors.
 CC Genetic variants of H4 can be used to diagnose an H4 associated disease
 CC as described above. The H4 receptor polynucleotide is useful to treat or
 CC prevent a disorder associated with the function of H4 in peripheral blood
 CC leukocytes. The present sequence represents the human histamine H4
 CC receptor protein

XX Sequence 390 AA;

Query Match 64.3%; Score 1308.5; DB 5; Length 390;
 Best Local Similarity 65.1%; Pred. No. 1,9e-128;
 Matches 253; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFPLMSLAIAMKGNVVIATFVDRNLHRSNYFFLNLAIDFFV 63
 DB 5 NSTIINSLSTRVTLAFEMSLVAFAMIGNALVILAFVDRNLHRSNYFFLNLAIDFFV 64
 QY 64 GATAIPLYIPSSLTWTMSGKACVFMILTDTYLLCTASVNVIVISYRYSVSNVAYRA 123
 DB 65 GVISIPLYIPHTLFEMDFGEICVFWLTDTYLLCTASVNVIVISYRYSVSNVAYRT 124
 QY 124 QHSGTWKIATQWAVMIFSFMTNGPMILISDSQNSTTECEPGFLKKWFALPTSLLEFL 183
 DB 125 QHTGVUKITVTLMAVAVWVLAFLVNGPMILVSESKWDESECEPGFSFWYLAITSFLEFV 184
 QY 184 IPIILVAVFAHIIYWSIMKREKLSRCLSHPVLPDSSSSDHGSCRODPDSRATLPARKE 243
 DB 185 IPIILVAVFMNIIYWSIMKRDHLSCQSHPLTA-VSSNICGHSFGRSLSSRSLSASTE 243
 QY 244 TTASLSDSKRRKSSLLPSIRAYKNSNVIVASKGFLSHSLSLALQOEHELEPRARLAK 303
 DB 244 VPASFSEHRRKSSLLMFSSRTKNSNTIASKMGFSQSDSVLHOREHELEPRARLAK 303
 QY 304 SLAILLAFAFICWAPYSLTIVISFPERNLTSTWHTAFMLQWPNFVNPFLYPLCHK 363
 DB 304 SLAILLGVAFCWAPYSLTIVISFYSATGPKSVWYRIAFWLQWPNFVNPFLYPLCHK 363
 QY 364 RFQKAFKLILPVRROSTP-PHNSISIT 389
 DB 364 RFQKAFKLIFCIKQPLPSQHSRSVSS 390

RESULT 12

AAU74906
 ID AAU74906 standard; protein: 390 AA.

XX AC AAU74906;

XX DT 09-APR-2002 (first entry)

XX DE Amino acid sequence of human G-protein coupled receptor TGR62 protein.

XX KW Human: G-protein coupled; receptor: GPCR; TGR62; kidney disease;
 KW signal transduction modulator; cerebral cavernous malformation;
 KW hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure;
 KW nephritis; hypertension; liver disease; cirrhosis; blood disorder;
 KW spleen-associated disorder; immune disorder.

XX OS Homo sapiens.

XX PN W0200200719-A2.

XX PD 03-JAN-2002.

XX XX

PF 25-JUN-2001; 2001WO-US020363.

XX 23-JUN-2000; 2000US-0213461P.

XX PA (TUL-) TULARIK INC.

XX PI Lin DC, Zhao J, Chen J, Cutler G;

XX DR WPI: 2002-147880/19.

XX DR N-PSDB; ABK12959.

XX PT New G-protein coupled receptor polypeptides, useful for identifying
 PT modulators of signal transduction for treating kidney disease,
 PT hyperlipidemia, obesity, dyslexia and cardiac myxoma.

PS Claim 26; Page 61; 78pp; English.

XX The present invention relates to a new G-protein coupled receptor (GPCR)
 CC polypeptide comprising greater than 70% amino acid sequence identity to
 CC the amino acid sequence of human GPCRs TGR62, TGR21, TGR130.1, TGR130.2,
 CC human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18 or
 CC 90% amino acid sequence identity to human novel edg receptor protein, as
 CC defined in the specification. The GPCR covalently linked to a solid phase
 CC is useful for identifying a compound that modulates signal transduction.
 CC The identified compounds are useful for treating kidney disease, cerebral
 CC cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac
 CC myxoma. The molecules of the invention are useful for diagnosing
 CC disorders or conditions such as kidney-related conditions or diseases
 CC such as renal failure, nephritis, nephrotic syndrome, asymptomatic
 CC urinary abnormalities, renal tubule defects, hypertension and
 CC nephrolithiasis, liver-related disease or condition e.g. cirrhosis,
 CC infiltrations, lesions, functional disorders and jaundice and spleen-
 CC associated disorders or conditions e.g. splenic enlargement, immune
 CC disorders, blood disorders and others. Modulation of the polypeptide of
 CC the invention is useful to treat or prevent any of the above conditions
 CC or diseases. The present amino acid sequence represents the human GPCR
 CC TGR62 protein of the invention. This sequence is one of seven novel G
 CC protein coupled receptors of the invention (AAU74904- AAU74911)

XX Sequence 390 AA;

Query Match 64.3%; Score 1308.5; DB 5; Length 390;
 Best Local Similarity 65.1%; Pred. No. 1,9e-128;
 Matches 253; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFPLMSLAIAMKGNVVIATFVDRNLHRSNYFFLNLAIDFFV 63
 DB 5 NSTIINSLSTRVTLAFEMSLVAFAMIGNALVILAFVDRNLHRSNYFFLNLAIDFFV 64
 QY 64 GATAIPLYIPSSLTWTMSGKACVFMILTDTYLLCTASVNVIVISYRYSVSNVAYRA 123
 DB 65 GVISIPLYIPHTLFEMDFGEICVFWLTDTYLLCTASVNVIVISYRYSVSNVAYRT 124
 QY 124 QHSGTWKIATQWAVMIFSFMTNGPMILISDSQNSTTECEPGFLKKWFALPTSLLEFL 183
 DB 125 QHTGVUKITVTLMAVAVWVLAFLVNGPMILVSESKWDESECEPGFSFWYLAITSFLEFV 184
 QY 184 IPIILVAVFAHIIYWSIMKREKLSRCLSHPVLPDSSSSDHGSCRODPDSRATLPARKE 243
 DB 185 IPIILVAVFMNIIYWSIMKRDHLSCQSHPLTA-VSSNICGHSFGRSLSSRSLSASTE 243
 QY 244 TTASLSDSKRRKSSLLPSIRAYKNSNVIVASKGFLSHSLSLALQOEHELEPRARLAK 303
 DB 244 VPASFSEHRRKSSLLMFSSRTKNSNTIASKMGFSQSDSVLHOREHELEPRARLAK 303
 QY 304 SLAILLAFAFICWAPYSLTIVISFPERNLTSTWHTAFMLQWPNFVNPFLYPLCHK 363
 DB 304 SLAILLGVAFCWAPYSLTIVISFYSATGPKSVWYRIAFWLQWPNFVNPFLYPLCHK 363
 QY 364 RFQKAFKLILPVRROSTP-PHNSISIT 389
 DB 364 RFQKAFKLIFCIKQPLPSQHSRSVSS 390

RESULT 13
 ABG71960
 ID ABG71960 standard; protein; 390 AA.
 XX
 AC ABG71960;
 XX
 DT 28-JAN-2003 (first entry)
 XX
 DE Human G-protein coupled receptor AXOR35.
 XX
 KM Human; receptor; G-protein coupled receptor; AXOR35; lymphocyte;
 KM macrophage; eosinophil; neutrophil; infection; transplant rejection;
 KM gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;
 KM Crohn's disease; irritable bowel syndrome; vomiting; inflammation;
 KM atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;
 KM psoriasis; urological disease; urinary retention; cardiovascular disease;
 KM myocardial infarction; hypertension; hypertension; pulmonary disorder;
 KM chronic obstructive pulmonary disease; cough; renal disease;
 KM renal ischemia; arteriosclerosis; atherosclerosis; psychosis;
 KM neurological disorder; migraine; anorexia; anxiety; schizophrenia;
 KM dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;
 KM gratic versus host disease; osteoporosis.
 XX
 OS Homo sapiens.
 XX
 PN US2002137054-A1.
 XX
 PD 26-SEP-2002.
 XX
 PF 20-JUL-2001; 2001US-00910411.
 XX
 PR 02-NOV-1999; 99US-00431898.
 PR 03-FEB-2000; 2000US-00497790.
 PR 20-OCT-2000; 2000US-00693761.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 XX
 PI Aubert KM, Bergema DJ, Fitzgerald L, Graybill TL, Li X,
 PI Michalovich D, Morrow DM, Zhu Y;
 DR N-PSDB; ABS57063.
 DR WPI, 2003-074982/07.
 XX
 PT Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for
 PT treating infections, gastrointestinal disorders, autoimmune disorders,
 PT urological diseases, cardiovascular diseases and cancer.
 XX
 PS Claim 1; Page 22; 24pp; English.
 XX
 CC The invention relates to an isolated G-protein coupled receptor
 CC polypeptide, AXOR35, (and its homologues, variants, complements and RNA
 CC equivalents). Also included are an anti-AXOR35 antibody, an AXOR35
 CC expression vector, producing a recombinant host cell by introducing the
 CC vector into a cell such that the host cell produces AXOR35, a membrane of
 CC the host cell expressing AXOR35, identifying/screening for agonists or
 CC antagonists of AXOR35 and inhibiting or promoting the function of
 CC lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,
 CC by administering to the patient AXOR35 agonists or antagonists. The
 CC agonist or antagonist identified is useful for treating a disease such as
 CC asthma, or for inhibiting or promoting the function of lymphocytes,
 CC macrophages, eosinophils, or neutrophils in diseased tissue such as an
 CC asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays,
 CC for identifying compounds that are agonists or antagonists of AXOR35, as
 CC vaccines, or for treating infections (bacterial, fungal, protozoan or
 CC viral infections), transplant rejection, gastrointestinal disorders (such
 CC as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),
 CC irritable bowel syndrome, vomiting, inflammation (such as atopic
 CC dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,
 CC psoriasis), urological diseases (such as urinary retention),
 CC cardiovascular diseases (such as myocardial infarction), hypertension,

CC hypertension, pulmonary disorders (such as chronic obstructive pulmonary
 CC disease), cough, renal diseases (such as renal ischaemia),
 CC arteriosclerosis, atherosclerosis, psychotic and neurological disorders
 CC (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such
 CC as Parkinson's disease), cancer, obesity, stroke, septic shock, gratic
 CC versus host disease and osteoporosis. The present sequence represents
 CC human AXOR35
 CC
 XX
 SQ Sequence 390 AA;
 XX
 Query Match 64.3%; Score 1308.5; DB 6; Length 390;
 Best Local Similarity 65.1%; Pred. No. 1.9e-126;
 Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;
 XX
 QY 5 NSTILMT-SIKISTFLMSLALAIAMLGNVYLAIFIYDRNLRRSNRYFLMLAIADFFV 63
 DB 5 NSTILMSSTRVTLAFPMFLVFAIMLGNALVILAFVDKILRRSSYFLMLAISDFV 64
 QY 64 GAIALPLYIPSSLIYWTSGKQACVFWLITDYLLCTASVYNIYLISYDRQSVSNMAYRA 123
 DB 65 GVISIPLYIPHTLFEMDRGKEICVFWLITDYLLCTASVYNIYLISYDRYSVSNMAYRT 124
 QY 124 QHSGTWKIAIQWVAWVITSPFMNGPMILISDQWQSTCECEGFLKWTYFALPTSLLEFL 183
 DB 125 QHTGVAKIVTLVWVAWVLAFLVNGPMILVBSKQEGCEGFFSEWYLAITSELEFV 184
 QY 184 IPILVAFYSAHIYWSLWKREKLSRCLSHPVLPSSDSSDHGSCRODPDSRATLPARKE 243
 DB 185 IPVILVAFYFNMYSLWKRRHLSRCQSHPGTLA-VSSNICHSRGRSLRSRSASRE 243
 QY 244 TTASLGSQSKRRKSSLLPSIRAYKSNVYIASWGFLLSHSDSLAQOREHIELFRACKLAK 303
 DB 244 VPASFHSERQRKSSLMFSSTKKNNSNTIASWGSFSDSVALQREHVELLRARLAK 303
 QY 304 SLATLLAFATCMARYSLTTVYISFEPERNLTKSTWYHTAFPLQWENSFVNPLVPLCKK 363
 DB 304 SLATLLGVAVCAWAPYSLFTVLSFYSSATGKSVYRIAFWLPQWNSFVNPLVPLCKK 363
 QY 364 RFQKAFKILPVRRQSTP-PHNRISIST 389
 DB 364 RFQKAFKILFCIKKQPLPSQHSRSYVS 390
 XX
 RESULT 14
 ABU92265
 ID ABU92265 standard; protein; 390 AA.
 XX
 AC ABU92265;
 XX
 DT 16-JUL-2003 (first entry)
 XX
 DE Human G protein-coupled receptor hRUP7.
 XX
 PN US2003017528-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 06-JUN-2001; 2001US-00875076.
 XX
 PR 20-NOV-1998; 98US-0109213P.
 PR 16-FEB-1999; 99US-0120416P.
 PR 26-FEB-1999; 99US-0121852P.
 PR 12-MAR-1999; 99US-0123946P.
 PR 12-MAR-1999; 99US-0123949P.
 PR 28-MAY-1999; 99US-0136435P.
 PR 28-MAY-1999; 99US-0136437P.
 PR 28-MAY-1999; 99US-0136439P.

PR 28-MAY-1999; 99US-0136567P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-0141448P.
PR 28-SEP-1999; 99US-0156333P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156634P.
PR 12-OCT-1999; 99US-00417044.
XX
XX (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LIAM/) LIAM C W.
PA (LINI/) LIN I.
XX
XX Chen R, Dang HT, Liaw CM, Lin I;
XX WPI, 2003-428952/40.
XX N-PSDB; ACA93262.
XX
XX Novel endogenous, orphan, human G protein-coupled receptors useful for
PT identification of modulators of the receptor and as research tools for
PT understanding the role of the receptor in human body.
XX
XX Claim 26; Page 23; 54pp; English.
XX
XX The invention relates to a human G protein-coupled receptor (GPCR)
CC appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named
CC hARE-3, hARE-4, hARE-5, hRUP3, hRUP5, hRUP6, hRUP7, hGPCR27, hARE-1, hARE
CC -2, hPER1, hG2A, hCHN3, hCHN4, hCHN5, hCHN6, hCHN8, hCHN9, hCHN10 and hRUP4.
CC Also included are a plasmid comprising a vector and one of the cDNAs
CC above and a host cell comprising the plasmid. The GPCRs are useful for
CC the direct identification of candidate compounds as inverse agonists,
CC agonists or partial agonists. In vitro and in vivo systems incorporating
CC GPCRs is useful for elucidating and understanding the roles these
CC receptors play in the human condition, both normal and diseased, as well
CC as understanding the role of constitutive activation as it applies to
CC understanding the signalling cascade. The cDNAs are useful for making a
CC probe for dot-blot analysis against tissue mRNA and/or RT-PCR
CC identification of the expression of the receptor in tissue samples. The
CC present sequence represents a GPCR of the invention
XX
XX Sequence 390 AA;
SQ
Query Match 64.3%; Score 1308.5; DB 6; Length 390;
Best local similarity 65.1%; Pred. No. 1.9e-128;
Matches 252; Conservative 46; Mismatches 84; Indels 3; Gaps 3;
QY 5 NSTIALT-SIKSLTFLMSILAIAMLGNNVILAFIVDRNLHRSNYPLNLAIADFFV 63
DB 5 NSTINLSLSTRVTLAFPMGLVAFAMLGNALVILAFVVDKLNLRHSYPLNLAIADFFV 64
QY 64 GAIAIPLYPSLTITTSKQACVFWLITDYLLCTASVNIYVILISIDRYOSVSNAYWYRA 123
DB 65 GVISILPLYPHLTLEWDFGKEICVFWLITDYLLCTASVNIYVILISIDRYOSVSNAYWYR 124
QY 124 OHSGTKIKITOMAVWIFSPMTNGPMILISDSMONSTTECEPGLKMWYFALTLSTLEPT 183
DB 125 QHGVUKITITLWAAVLAFLVNGPMILVSESKWDESECEPFPSEWYLAITSELEFY 184
QY 184 IPIILVAYSAAHLYMSLWKRKELSRCLSHPEVLPSDSSSDHGHSCRDPPSRATLPARKE 243
DB 185 IPIILVAYFNMNIYMSLWKRKDHLSRCOSHGLTA-VSSNLCGHSFGRSLRSLSASTE 243
QY 244 TTRSLGSDSRKRSLLPISIRAYKSNVIAASKGFLSHSGSLAQOREHIELEFRARKLAK 303
DB 244 VPSFSFHSRRRRSSSLMFSSRTKNSNTJASKGFSQSDSVALLHREHVELLRARLAK 303
QY 304 SLAIIAAAFICAPYSLTIVISFPERLUTKSTWHTAFMLQWFSFVNPFLYPLCHK 363
DB 304 SLAIIIGVPAVCWAPSLFTIVISFSSAAGPSSWYRIAFWLOMNSFNPFLYPLCHK 363
QY 364 RFQKAFKLILPVRRQSTP-PHNSISIT 389

DB 364 RFQKAFKLIFCIKKOPLPSQHSRVS 390
RESULT 15
ID ABP81727 standard; protein; 390 AA.
XX
XX ABP81727;
AC
XX 04-MAR-2003 (first entry)
DT
XX Human histamine H4 receptor protein SEQ ID NO:629.
DE
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KM G protein-coupled receptor modulator; antibody; immune-related disease;
KM growth-related disease; cell regeneration-related disease; AIDS; cancer;
KM immunological-related disease; cell proliferative disease; autoimmune disease;
KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KM ulcer.
XX
XX Homo sapiens.
OS
XX WO200261087-A2.
PN
XX 08-AUG-2002.
PD
XX
XX 19-DEC-2001; 2001MO-US050107.
PF
XX
XX 19-DEC-2000; 2000US-0257144P.
PR
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
PA
XX Burner GC, Roush CL, Brown JP;
PI
XX WPI, 2003-046718/04.
DR
XX N-PSDB; AB242573.
DR
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
XX Disclosure; Fig 1; 523pp; English.
PS
XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnoses. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2005, 19:13:41 ; Search time 4456 Seconds
(without alignments)
4230.045 Million cell updates/sec

Title: US-10-626-398-10

Perfect score: 2036
Sequence: 1 MLIANNSTALTSIKSLTFL.....LKILPVRQSTPPHNRISST 369

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool.p/US10626398/runat_02082005.155808.2915/app_query.fasta_1.583
-DB=GenEmbl -QFMT=fastab -SUFFIX=xrge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptco NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10626398@cgn2.1_15600@runat_02082005.155808.2915 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WMAP TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pac: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_seg: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB ID	Description
No.					
1	2025	99.5	1451	10	AF358858 Cavia por
2	1310.5	64.4	1173	9	AY008280 Homo sapi
3	1308.5	64.3	1173	6	ARI42850 Sequence
4	1308.5	64.3	1173	6	AR391860 Sequence

5	1308.5	64.3	1173	6	AX109119 Sequence
6	1308.5	64.3	1173	6	AX139113 Sequence
7	1308.5	64.3	1173	6	AX301763 Sequence
8	1308.5	64.3	1173	6	BD015847 Novel pol
9	1308.5	64.3	1173	9	AF307973 Homo sapi
10	1308.5	64.3	1173	9	AF325356 Homo sapi
11	1308.5	64.3	1173	9	AF329449 Homo sapi
12	1308.5	64.3	1173	9	AF336745 Homo sapi
13	1308.5	64.3	1173	9	HS298292 Homo sapi
14	1308.5	64.3	1173	9	AX376577 Sequence
15	1308.5	64.3	1300	6	AX301229 Sequence
16	1308.5	64.3	1312	6	BD095598 Novel gua
17	1308.5	64.3	1312	9	AB045370 Homo sapi
18	1308.5	64.3	1316	9	BC069136 Homo sapi
19	1308.5	64.3	3569	6	AX549343 Sequence
20	1308.5	64.3	3569	9	AF312230 Homo sapi
21	1306.5	64.2	1227	6	BD097512 Novel gua
22	1306.5	64.2	1265	9	AB044934 Homo sapi
23	1244	61.1	1538	10	AF358859 Sequence
24	1235.5	60.7	1593	10	AF358860 Sequence
25	1221.5	60.0	1291	4	AB053300 Sus scrofa
26	869.5	42.7	14055	9	AC007922 Homo sapi
27	869.5	42.7	166206	2	AC009668 Homo sapi
28	869.5	42.7	167296	2	AP002507 Homo sapi
29	869.5	42.7	169144	9	AC090244 Homo sapi
30	869.5	42.7	184938	2	AP002476 Homo sapi
31	869.5	42.7	193779	2	AP001327 Homo sapi
32	819.5	40.3	199837	10	AC131672 Mus muscu
33	806.5	39.6	236694	2	AC118386 Rattus no
34	698	34.3	1249	10	AF267538 Cavia por
35	694.5	34.1	1239	6	E359806 Novel guano
36	694.5	34.1	1239	6	AR559670 Sequence
37	694.5	34.1	1242	10	AY009371 Rattus no
38	694.5	34.1	2700	6	E359809 Novel guano
39	694.5	34.1	2700	6	AR559673 Sequence
40	693	34.0	1339	10	AF267537 Cavia por
41	689.5	33.9	1335	6	ARI42850 Sequence
42	689.5	33.9	1335	6	ARI35733 Sequence
43	689.5	33.9	1335	6	BD235873 Isolated
44	689.5	33.9	1335	6	AR217195 Sequence
45	689.5	33.9	1335	6	BD086286 G protein

ALIGNMENTS

RESULT 1
AF358858
LOCUS AF358858 1451 bp mRNA linear ROD 02-SEP-2001
DEFINITION Cavia porcellus histamine H4 receptor mRNA, complete cds.
ACCESSION AF358858
VERSION AF358858.1 GI:15420532

KEYWORDS
SOURCE
ORGANISM
Cavia porcellus

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 1451)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.

JOURNAL
AUTHORS
TITLE
2 (bases 1 to 1451)
Comparison of human, mouse, rat, and guinea pig histamine H4
receptor suggests substantial species variation

REFERENCE
AUTHORS
TITLE
Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
CA 92121, USA

FEATURES
source
1..1451
Location/Qualifiers

CDS
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/db_xref="taxon:10141"
101..1270

/note="G-protein-coupled receptor"
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/protein_id="AAK97379.1"
/db_xref="GI:15420533"
/translation="MLANNSTIALUTSISLTFPLMSLLAIAIMGNVVIILAFYDRN
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TECEGFLPKWYFALPTSLBELIPILVAVFSAHYWSIMREKLSCLSPVLPD
SSSDHSGSCRODPDSRATLPARKETSLGSKSRKSLIFSIKAYKSNVIAASKM
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ORIGIN

Alignment Scores:

Pred. No.: 2,426-166 Length: 1451
Score: 2025.00 Matches: 388
Percent Similarity: 99.74% Conservative: 0
Best Local Similarity: 99.74% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: Gaps: 0

US-10-626-398-10 (1-389) x AFS58858 (1-1451)

QY 1 MetLeuAlaAsnSerThrIleAlaIeuThrSerIleuYsIleSerIeuThrPheIeu 20
Db 101 ATGTTGGCAAAATMACAGTACATCCCTTAACATTAATTAATTTCTTGACATTTTAA 160
QY 21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValIleValIleLeuAlaPheIle 40
Db 161 ATGCTTTACTACGCTAATGCTTAATGTTAGGCAATGCTGCTGCTTACTTTTACTTTATT 220
QY 41 ValAspArgAsnLeuAlaArgHisArgSerAsnYrPhePheLeuAsnLeuAlaIleAlaAsp 60
Db 221 GTGGACAGAAATCTTAGACATGAGATTAATCTTTTCTTAACCTTGCCATTCAGAC 280
QY 61 PhePheValGlyAlaIleAlaIleProIeuYrIleProSerSerIeuThrYrTrpThr 80
Db 281 TTTCTTTGGGGCAATTCATCTCTGTACATACCTTCCTCGCTACATTCAGGACT 340
QY 81 SerGlyValGlnAlaCysValPheTrpLeuIleThrAspYrLeuLeuCysThrAlaSer 100
Db 341 TCTGAAAGCAAGCTTGCTGATATTTGGCTCATTCATCTATCTTTTATGACACACTT 400
QY 101 ValYrAsnIleValIleuIleSerYrAspArgYrGlnSerValSerAsnAlaValTrp 120
Db 401 GTGATATATATGCTCCTCATGACGATCGCTACGATCGCTCAATGCGGTGG 460
QY 121 TyrArgAlaGlnHisSerGlyThrTrpYsIleAlaThrGlnMetValAlaValTrpIle 140
Db 461 TATAGAGCTCAGCACTCGGACCGCGAAATTTGCTACTCAGATGCTGCTGTTGGATA 520
QY 141 PheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThr 160
Db 521 TTTCTCTTCATACAAATGGGCCGATGATTCGATTTTCAGACTCTTGGCAGATATGCCACT 580
QY 161 ThrGlnCysGluProGlyPheLeuYsYrTrpYrPheAlaIleuProThrSerIeuLeu 180
Db 581 ACAGAAATGGAACCTGGATTTTAAAAAGGTGACTTGGCTCCCTCAACATCATTAATTC 640
QY 181 GluPheLeuIleProIleLeuLeuValAlaYrPheSerAlaHisIleYrTrpSerIeu 200
Db 641 GAATTCCTGATCCCATCTTGTAGTGGTTAATTTTCAGGGCCCAATATTCAGGAGCTCG 700
QY 201 TrpLysArgGluLeuLeuSerArgCysLeuSerHisProValIeuProSerAspSerSer 220
Db 701 TGGAAAGCAGAGAACTGAGCAGGTGCTCAGCCACCTGTACTCCCTCTGACTCTTCC 760
QY 221 SerSerAspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrIeuProAla 240
Db 761 AGCAGTGAACACGAGCACTCCTGACAGACAGACCCGATTCAGAGGCGACTCTGCACAGA 820
QY 241 ArgLysGluThrThrAlaSerIeuLeuYsSerAspYsSerArgLysSerSerIeuLeu 260

Db 821 CGGAAGAAACACTGCTCTCTGTTGCACAGACATCGAGAGAAAGCAGTCTCTTG 880
QY 261 ProSerIleArgAlaYrLeuAsnSerAsnValIleAlaSerIleMetGlyPheLeuSer 280
Db 881 TTTTCCATTAAGAGCTTACAAAGACGACATGATGCTCTCCAAATAGGCTTCTCTCC 940
QY 281 HisSerAspSerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgLys 300
Db 941 CACTCAGATTCCTCGGCTCTCAGAAAGGAACATACGAATCTTTTCAGAGCCAGGAAA 1000
QY 301 LeuAlaYsSerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProYrSer 320
Db 1001 TTAGCCAAATCAGCGCCATCTCTTCACACTTTTGCCATTTGCGGCTCCATATCA 1060
QY 321 LeuThrTrValIleYrSerPhePheProGluArgAsnLeuThrLysSerThrTrpYr 340
Db 1061 CTGACTACAGTATCTACTCTATTTTCTGAAAGAACTTGACTTAATCAACCTGTTAC 1120
QY 341 HisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuYrProIeu 360
Db 1121 CATACGCTTTTGCTGCTCAGAGGTTCAATTCCTTGTAAATCCCTTTTGTATCATTTG 1180
QY 361 CysHisLysArgPheGlnLysAlaPheLeuYsIleLeuProValArgArgLysSerThr 380
Db 1181 TGTACAAACGTTTTCAGAAAGCTTTCCTGAATAATCTCTGTGAGAAAGCAATCCAG 1240
QY 381 ProProHisAsnArgSerIleSerThr 389
Db 1241 CCACCACAAACCGCTCAATATCCACT 1267

RESULT 2
AY008280 1173 bp mRNA linear PRI 15-MAR-2004
LOCUS Homo sapiens histamine receptor H4 (H4) mRNA, complete cds.
DEFINITION
ACCESSION AY008280
VERSION AY008280.1 GI:15822540
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and
Nguyen,T., Shapiro,D.A., George,S.R., Setola,V., Lee,D.K.,
Cheng,R., Rausser,L., Lee,S.P., Lynch,K.R., Roth,B.L. and
O'Dowd,B.F.
TITLE Discovery of a novel member of the histamine receptor family
JOURN. Mol. Pharmacol. 59 (3), 427-433 (2001)
MEDLINE
PUBMED 11179435
REFERENCE
AUTHORS Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and
O'Dowd,B.F.
TITLE Discovery of H4, a Novel Histamine Receptor
JOURNAL Unpublished
AUTHORS Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and
O'Dowd,B.F.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2000) Pharmacology, University of Toronto, 8
Raddle Creek Rd., Rm. 4353, Toronto, Ont M5S 1A8, Canada
FEATURES
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1..1173
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NYVLISYRVLISVSNVAVSRVOTGVLTAKLVAVWVLAFLVNPMLVSVSMDE
GSECEGFSEFSEYI LAITSLEFEVIPIVLVAFNMNIVMSLGRDLSRQSGPGLTA
VSNICGHSRFRSLSRSLASSTEVPAFSPHSRORSSLSMRSTKNSNTASKM
GSPSODSVALHOREVELLRARLAKSLAILLGVAFCVAPSLFTIYLSFSSATG
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ORIGIN

Alignment Scores:

Pred. No.:	2,43e-104	Length:	1173
Score:	1310.50	Matches:	253
Percent Similarity:	76.98%	Conservative:	48
Best Local Similarity:	64.71%	Mismatches:	87
Query Match:	64.37%	Indels:	3
DB:	9	Gaps:	3

US-10-626-398-10 (1-389) x AY008280 (1-1173)

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QY 1 MetLeuAlaAenAnSerThrIleAlaLeuThr---SerIleYsileSerleuThrPhe 19
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QY 20 LeuMetSerleuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPhe 39
DB 61 TTTATGCTCTTAGCTTAGCTTTTGCTATATAGTGAATGCTTAGCATTTAGCTTTT 120
QY 40 IleValAspArgAsnLeuArgHisArgSerAsnTyrrPhePheLeuAenLeuAlaIleAla 59
DB 121 GTGCTGACAAACCACTTAGACATCGAAGTAGTATTATTTTCTTAAGTGGCACTCT 180
QY 60 AspPhePheValGlyAlaIleAlaIleProleuTyrrIleProserleuThrTyrrTyr 79
DB 181 GACTTCTTGTTGGTGGATCTCCATTCCTTTGACATCCCTCAACGGCTGTCGAATGG 240
QY 80 ThrSerGlyYsleGlnAlaCyseValPheTrpLeuIleThrAspTyrrleuLeuCyseThrAla 99
DB 241 GATTTTGAAAGAAATCTGTGATTTTGGCTCACTACTACATCTGTATGTACGCA 300
QY 100 SerValTyrrAsnIleValIleuSerTyrrAspArgTyrrGlnSerValSerAsnAlaVal 119
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QY 120 TrpTyrrArgAlaGlnHisSerGlyThrTrpYsileAlaThrGlnMetValAlaValTyr 139
DB 361 TCTTATAGAACTCAACATCTAGGGGTCTGAAGATTGTACTGTGATGGTGGCGTTGG 420
QY 140 IlePheSerPheMetThrAsnGlyProMetIleleuIleSerAspSerTrpGlnAsnSer 159
DB 421 GTGCTGCGCTCTTAGAATGGGCCAATGATTTCTATTTCAAGATCTTGAAAGATGAA 480
QY 160 ThrThrGluCyseGlnProGlyPheLeuYsleTrpTyrrPheAlaLeuProThrSerLeu 179
DB 481 GGTAGTGAATGTAACTGGAATTTTTCGGAATGTGATCCCTGGCATCAACATCTTC 540
QY 180 LeuGlnPheLeuIleProIleLeuLeuValAlaTyrrPheSerAlaHisIleTyrrTrpSer 199
DB 541 TTGGAATTCGTGATCCAGTCACTTATGTGCTTATTTCAACATGAATATTTATTTGGAGC 600
QY 200 LeuTrpTyrrArgGlnYsleuSerAsnGlyLeuSerHisProValleuProserAspSer 219
DB 601 CTGTGGAAGGTATCATCTCAGTAGGTGCAAGCCATCTGAGACTGCTGCT--GTC 657
QY 220 SerSerSerAspHisArgYsleSerCyseArgGlnAspProAspSerArgAlaThrLeuPro 239
DB 658 TCTTCCAACTCTGTGACATCTATTCAGAGTAGACATCTTCAGAGAAATCTCTTTCT 717
QY 240 AlaArgYsleGlnThrThrAlaSerLeuGlySerAspYsleSerArgArgYsleSerSerLeu 259
DB 718 GCATGACAGAAAGTCTCTGATCTTTCATTCAAGACAGACAGAGAAAGAGTAGTCTC 777

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QY 260 LeuProSerIleArgAlaTyrrYsAsnSerAsnValIleAlaSerYsMetGlyPheLeu 279
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QY 280 SerHisSerAspSerleuAlaLeuGlnGlnArgGlnHisIleGlnLeuPheArgAlaArg 299
DB 838 TCCCATTCAGATCTGTAGCTCTTCCACCAAGGAACATGTTCACTGCTTAGACGACAG 857
QY 300 LysLeuAlaYsSerleuAlaIleLeuLeuAlaAlaPheAlaIleCyseTrpAlaProTyrr 319
DB 898 AGATTAGCCAAAGTCACTGCGCATTTCTTAGAGGCTTTTGCTGCTTGGCGGCTCATAT 957
QY 320 SerLeuThrThrValIleTyrrSerPhePheProGlnArgAsnLeuThrYsSerThrTrp 339
DB 958 TCTCTGTTCCAAATGTGCTTCTTATTTATCTTCCACCAACAGCTCTTAATACATTTGG 1017
QY 340 TyrrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrrPro 359
DB 1018 TATAGAAATGCAATTTGGCTTCAAGTGTCAATTCCTTTGTCAATCCTTTTGTATCCA 1077
QY 360 LeuCyseHisLysArgPheGlnLysAlaPheLeuYsIleLeuProValArgArgGlnSer 379
DB 1078 TTGCTGCACAGCGCTTTCAAAAGCCTTCTTGAATAATTTTGTATAAAGCAACCT 1137
QY 380 ThrPro---ProHisAsnArgSerIleSerThr 389
DB 1138 CTACCATTCACACACAGTGGTCAATGATCTTCT 1170

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RESULT 3
LOCUS AR142850 1173 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6204017.
ACCESSION AR142850
VERSION AR142850.1 GI:15104136
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
Umland,S.P. and Wang,S.
TITL Polynucleotide encoding a histamine receptor
JOURNAL Patent: US 6204017-A 1 20-MAR-2001;
FEATURES
Source 1..1173
location/Qualifiers
/organism="unknown"
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ORIGIN

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Percent Similarity:	77.52% <td>Conservative:</td> <td>48 </td>	Conservative:	48
Best Local Similarity:	65.12% <td>Mismatches:</td> <td>84 </td>	Mismatches:	84
Query Match:	64.27% <td>Indels:</td> <td>3 </td>	Indels:	3
DB:	6 <td>Gaps:</td> <td>3 </td>	Gaps:	3

US-10-626-398-10 (1-389) x AR142850 (1-1173)

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QY 5 AsnSerThrIleAlaLeuThr---SerIleYsileSerleuThrPheLeuMetSerLeu 23
DB 13 AATAGCAACATCAATTTATATCAAGACATCGTTCATTAGCATTTTATATGCTTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTGCTATATGCTTAGAAGAAATGCTTGTGCTATTTAGCTTTTGGTGGACAAA 132
QY 44 AsnLeuArgHisArgSerAsnTyrrPhePheLeuAsnLeuAlaIleAlaAspPhePheVal 63
DB 133 AACCTTAGACATGGAAGTGAATTTTCTTAACTTGGCCATCTGACTCTCTTTGTG 192
QY 64 GlyAlaIleAlaIleProleuTyrrIleProserleuThrTyrrTrpThrSerGlyYs 83

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Db      193 GGTGGATGATCCATTCCTTTGATACATCCCTCACACCTCTTGGAAAGGATTTTGGAAAG 252
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Db      253 GAAATCTGTGATTTTGGCTCACTACTGATCTATCTTTATGACACACTGTATATATAC 312
Qy      104 IleValIleuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrPyrArgAla 123
Db      313 ATTGCCCTCATGAGTATGATCATCTGTGACGTCTCAAAATGCTGTGCTTATGAACT 372
Qy      124 GlnHisSerGlyThrTrpValIleAlaThrGlnMetValAlaValTyrIlePheSerPhe 143
Db      373 CAACATACAGGGGCTCTGGAAGATGTGTACTGTGATGTGCGCTGTGGGCTGGCCCTTC 432
Qy      144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrGlnCys 163
Db      433 TTAGTGCATAGGGCCCAATGATTTCTAGTTTCAAGATCTTGGAAAGATGAAGTGTGAAATCT 492
Qy      164 GluProGlyPheLeuValSerTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db      493 GAACCTGATTTTTCGGAATGTGTACATCTTGCCATCATCATCTTTGGAAATTCGTG 552
Qy      184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpValArg 203
Db      553 ATCCAGATCATCTTATGTCGCTTATTTCAACATGAATATTATTTGAGCCTGTGGAAAGCCT 612
Qy      204 GluPylSerSerCysLeuSerHisProValIleProSerAspSerSerSerAsp 223
Db      613 GATCATCTCATAGTAGGTGCCAAAGCCATCTTGACATGACTGCT---GTCTCTTCCAACATC 669
Qy      224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgIysGlu 243
Db      670 TGTGGACACTCATTTCAAGAGTACTATCTCAAGAGATCTCTTCTGCATCGACAGA 729
Qy      244 ThrThrAlaSerLeuGlySerAspIysSerArgArgIysSerSerLeuLeuProSerIle 263
Db      720 GTTCTGTCATCTTTTCATTCAAGAGACAGAGAGAGAAAGATGTCATGTTTCTCTCA 789
Qy      264 ArgAlaTyrLeuAsnSerAsnValIleAlaSerIysMetGlyPheLeuSerHisSerAsp 283
Db      790 AGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTCTCTCCCAATCAAGT 849
Qy      284 SerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgIysLeuAlaIys 303
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Qy      304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysThrAlaProTyrSerLeuThrThr 323
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Qy      324 ValIleTyrSerPhePheProGluArgAsnLeuThrIleSerThrTrpTyrHisThrAla 343
Db      970 ATTGTCCTTCAATTTTATTCCTCAGCAAGACAGGCTCAAAATCACTTTGGATATGAAATGCA 1029
Qy      344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuGlyHisIys 363
Db      1030 TTTTGGCTTCAGTGTGATTCCTTTGCAATCTCTTTGTATCCATTTGATCCATTTGTCACAAG 1089
Qy      364 ArgPheGlnValAlaPheLeuIysIleLeuProValArgArgGlnSerThrPro---Pro 382
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Db      1150 CACAGTCGCTCAGTATCTTCT 1170

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RESULT 4
AR391860 1173 bp DNA linear PAT 18-DEC-2003
LOCUS AR391860
DEFINITION Sequence 1 from patent US 6613533.
ACCESSION AR391860
VERSION AR391860.1 GI:40115588

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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monema,F.J., Morse,K.L.,
        Umland,S.P. and Wang,S.
TITLE Histamine receptor
JOURNAL Patent: US 6613533-A 1 02-SEP-2003;
FEATURES Location/Qualifiers
source 1..1173
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       /mol_type="genomic DNA"

Alignment Scores:
Pred. No.: 3,626-104 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
Db: 6 Gaps: 3

US-10-626-398-10 (1-389) x AR391860 (1-1173)
Qy      5 AsnSerThrIleValLeuThr---SerIleYsIleSerLeuThrPheLeuMetSerLeu 23
Db      13 AATACACAAATCAATTTATCATAGACACTGCTGTACTTATGCAATTTTATATGTCCTTA 72
Qy      24 LeuAlaIleAlaIleMetLeuGlyAsnValAlaValIleLeuAlaPheIleValAspArg 43
Db      73 GTAGCTTTTGCATATATATCTAGAAATGCTTGGTCATTTTGGCTTGTGTGACAA 132
Qy      44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
Db      133 AACCTTACATCGAAGTAGTATTTTCTTAACTTGCCATCTCTGACTCTTCTTGTG 192
Qy      64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpHisSerGlyIys 83
Db      193 GGTGGATCTCATTCCTTTGATACATCCCTCACAGCGTGTGGAATGGGATTTTGGAAAG 252
Qy      84 GlnAlaCysValPheThrLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
Db      253 GAAATCTGTGATTTTGGCTCACTGATCATCTTGTATATGACACATCTGTATATATAC 312
Qy      104 IleValIleuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrPyrArgAla 123
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Qy      124 GlnHisSerGlyThrTrpValIleAlaThrGlnMetValAlaValTyrIlePheSerPhe 143
Db      373 CAACATACAGGGGCTCTTGAAGATGTGTACTGTGATGTGCGCTGTGGGCTGGCCCTTC 432
Qy      144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrGlnCys 163
Db      433 TTAGTGCATAGGGCCCAATGATTTCTAGTTTCAAGGTCTTGGAAAGATGAAGTGTGAAATCT 492
Qy      164 GluProGlyPheLeuValSerTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db      493 GAACCTGATTTTTCGGAATGTGTACATCTTGCCATCATCATCTTTGGAAATTCGTG 552
Qy      184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpValArg 203
Db      553 ATCCAGATCATCTTATGTCGCTTATTTCAACATGAATATTATTTGAGCCTGTGAAAGCCT 612
Qy      204 GluPylSerSerCysLeuSerHisProValIleProSerAspSerSerSerAsp 223
Db      613 GATCATCTCATAGTAGGTGCCAAAGCCATCTTGACATGACTGCT---GTCTCTTCCAACATC 669
Qy      224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgIysGlu 243
Db      670 TGTGGACACTCATTTCAAGAGTACTATCTTCAAGAGATCTCTTCTGACATCGACAGA 729

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QY 244 ThrThAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuProSerIle 263
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QY 284 SerLeuAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 303
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QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThr 323
Db 910 TCATCGGCATCTCTTACAGGGGTTTTCGCTTTCGCGGCTCCATATTTCTGTTGACA 969
QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTyrTyrHisThrAla 343
Db 970 ATGTGCTTTTCAATTTATTCCTCAGCAACAGTCTTAAATCAGTTGGTATGAATTTGCA 1029
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Db 1030 TTTTGGCTTACAGGTTCATTCCTTGTCAATCCTTTTGTATCCATTTGTGTACAG 1089
QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgLysSerThrPro--Pro 382
Db 1090 CGCTTTCAAAAGGCTTTCTGAAATATTTTGTATTAATAAAGCAACCTACCATCAACA 1149
QY 383 HisAsnArgSerIleSerThr 389
Db 1150 CACAGTCGTCAGTATCTCT 1170

RESULT 5
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LOCUS AX109119
DEFINITION Sequence 1 from Patent WO0125432.
ACCESSION AX109119
VERSION AX109119.1 GI:13924093
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Behan, J. X., Hedrick, J. A., Laz, T. M., Monsma, F. J., Morse, K. L.,
AUTHORS Umland, S. and Wang, S.
TITLE Histamine receptor
JOURNAL Patent: WO 0125432-A 1 12-APR-2001;
SCHERING CORPORATION (US)
FEATURES
source location/Qualifiers
1.1173
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Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
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US-10-626-398-10 (1-389) x AX109119 (1-1173)

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QY 164 GluProGlyPheLeuLysTyrTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db 493 GAACTGGATTTTTCGGAATGTATCATCTTCCATCATCATCTTTGGAAATTCGTG 552
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DEFINITION    AX139113
ACCESSION     AX139113
VERSION       AX139113.1 GI:14274791
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SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE     1
AUTHORS       Peter, B. and O'Reilly, M.A.
TITLE         G-protein coupled receptor-like polypeptide
JOURNAL       Patent: EP 1096009-A 1 02-MAY-2001;
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Score:          1308.50        Matches:      252
Percent Similarity: 77.52%      Conservative: 48
Best Local Similarity: 65.12%    Mismatches:  84
Query Match:    64.27%         Indels:       3
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QY      184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTyrPheAsp 203
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ACCESSION     AX301763
VERSION       AX301763.1 GI:17382844
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ORGANISM      Homo sapiens
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REFERENCE     1
AUTHORS       Jones, P.G., Blatcher, M., Wu, S. and Pausch, M.H.
TITLE         Human histamine h4r receptor
JOURNAL       Patent: WO 0185786-A 1 15-NOV-2001;
              American Home Products Corporation
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ORIGIN
Alignment Scores:
Pred. No.:      3,62e-104      Length:      1173
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Percent Similarity: 77.52%      Conservative: 48
Best Local Similarity: 65.12%    Mismatches:  84
Query Match:    64.27%         Indels:       3
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DEFINITION Novel polypeptide.
ACCESSION BD015847
VERSION BD015847.1 GI:2256984
KEYWORDS JP 2001211889-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Peter B. and Olavlee, M.A.
TITLE Novel polypeptide
JOURNAL Patent: JP 2001211889-A 1 07-AUG-2001;
PUBLISHER PFIZER INC
COMMENT OS Homo sapiens (human)
PN JP 2001211889-A/1
PD 07-AUG-2001
PF 27-OCT-2000 JP 2000329359
PR 29-OCT-1999 GB 9925641.4, 20-APR-2000 GB 0009973:9 PI
BEAT PETER, MARK ANTONY OLAVLEE
PC C12N15/09, A61K38/00, A61K39/395, A61K48/00, A61P1/04,
PC A61P11/00,
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ORIGIN
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Pred. No.: 3,62e-104 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
Gaps: 3
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DEFINITION AF307973
ACCESSION AF307973
VERSION AF307973.1 GI:11141732
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 AUTHORS Zhu, Y., Michalovich, D., Wu, H.-L., Tan, K.B., Dytch, G.M.,
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 Herlitz, N.C., Vawter, L., Sarau, H.M., Ames, R.S., Davenport, C.M.,
 Hebl, P., Wilson, S., Bergsma, D.J. and Fitzgerald, L.R.
 Cloning, expression, and pharmacological characterization of a
 novel human histamine receptor
 JOURNAL Mol. Pharmacol. 59 (3), 434-441 (2001)
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REFERENCE 2 (bases 1 to 1173)
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Gustafsson, S.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M.,
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Cloning and characterization of a novel human histamine receptor
J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)
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MEDLINE
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Monsma, F.J., Jr., Wang, S., Behan, J., Laz, T.M., Greene, J. and
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Direct Submission
Submitted (15-DEC-2000) Human Genomics Research, Schering-Plough
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DB 1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 13

LOCUS HSA298292 1173 bp mRNA linear PRI 12-JAN-2002
DEFINITION Homo sapiens mRNA for histamine receptor H4 (HRH4 gene).
ACCESSION AJ298292
VERSION AJ298292.1 GI:18152452
KEYWORDS histamine receptor H4; HRH4 gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 O'Reilly M.A.
AUTHORS O'Reilly M.A.
TITLE Identification of a histamine H4 receptor on human eosinophils -
JOURNAL Role in eosinophil chemotaxis
REFERENCE 2 (bases 1 to 1173)
AUTHORS O'Reilly M.A.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2001) O'Reilly M.A., Discovery Biology, Pfizer
Ltd, Ramsgate Road, Sandwich, Kent, CT13 9NU, UNITED KINGDOM
FEATURES
source
1..1173
/organism="Homo sapiens"
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/cell_line="AML14.3D10"
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/function="G-protein coupled receptor"
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/evidence="experimental"
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GSECBGPFSEWYILAITSLFELFVILVAVENNIYVSLMKRDLRSQSHPGILTA
VSNICGHSFRRLISRSLASSTVYPASFSERQRKSLMFSRTKNSNTTISAKM
GSFSQSDSVLHOREHEVELLRARLKLALAILGVFAVCWAPYSLFTIVLSYSATG
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ORIGIN

Alignment Scores:
Pred. No.: 3 62e-104 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48

Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
DB: 9 Gaps: 3

US-10-626-398-10 (1-389) x HSA298292 (1-1173)

QY 5 AenSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
DB 13 AATACACATCAATTAATTAATCACTAGCACTCGTGTAATCTTGAATTTTATGTCCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAnValValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTGCTATATATCTAGGAATCTTGGTCATTTTGTGTGTGTGACAA 132
QY 44 AenLeuArgHisArgSerAsnTyrPhePheLeuAnLeuAlaIleAlaAspPheVal 63
DB 133 AACCTTAACATCGAAGTAGTATTTTCTTAACTTGCCATCTCTGACTTCTTTGTG 192
QY 64 GYAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpHisSerGlyLys 83
DB 193 GGTGTGATCTCATCTTGTGATCCCTCACAGCGCTGTTGAAATGGATTGGAAG 252
QY 84 GlnAlaCyValPheTrpLeuIleThrAspTyrLeuLeuCyStrpAlaSerValTyrAn 103
DB 253 GAATCTGTGATTTTGGCTCACTACTATCTGTATGTACAGCATCTGTATATAC 312
QY 104 IleValIleLysSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123
DB 313 ATTGCTCTCATGCTATGATGATGATGATCTGTACAGTCTCAATGCTGTGCTTATAGACT 372
QY 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
DB 373 CAACACTAGCGGGGCTTGAAGATTGTACTGTAGTGGGCCGTTGGGTGCGGCTTC 432
QY 144 MetThrAnGlyProMetIleLeuIleSerAspSerTrpGlnAnSerThrTrpGlyCys 163
DB 433 TTAAGAAATGGGCCAATATCTTACTGTACAGTCTTGAAGATGAAGATGAGTGTGATGT 492
QY 164 GluProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuGlnPheLeu 183
DB 493 GAACCTGATTTTTTTCGGAATGTATCACTCTGCCATCACTATCTTGGAAATTCGCG 552
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
DB 553 ATCCAGATCATCTAGTCGCTTATTTCAACATGAAATATTATTGAGCCTGTGAAGCGT 612
QY 204 GlnLysLeuSerArgCyLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 613 GATCATCTCAGTAGGTGCCAAAGCCATCTGTGACGTGACTGCT--GTCCTTCCAACTC 669
QY 224 HisGlyHisSerCyArgGlnAnPheProAspSerArgAlaThrLeuProAlaArgLysGlu 243
DB 670 TGTGACACTCATTTAGAGGTAGACTATCTTCAAGAGATCTCTTCTGACACAGAA 729
QY 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
DB 720 GTTCTGATCTCTTCATTCACAGAGACAGAGAAAGATGATCTCATGTTTCTCTCA 789
QY 264 ArgAlaTyrLysAnSerAnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATTAATGAAATCAATTCCTTCCAAATGGGTCTCTTCCCAATCCAGAT 849
QY 284 SerLeuAlaLeuGlnArgGlnHisIleGlnLeuPheArgAlaArgLysLeuAlaLys 303
DB 850 TTGTAGCTCTTACACAAAGGAAATGTGTAACCTGTAGAGCCAGAGATTAAGCCAAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaIaPheAlaIleCyStrpAlaProTyrSerLeuThrThr 323
DB 910 TCACGGCCATCTCTTAGGGGTTTGGCTGTGGTGGCCATATCTCTGTCACA 969
QY 324 ValIleTyrSerPhePheProGluArgAnLeuThrLysSerThrTrpTyrHisThrAla 343
DB 970 ATGGTCCTTCATTTTATCTCTCAGCACACAGGCTCTAAATCATTTGGATATGAATTGCA 1029

QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCySHisIlys 363
Db 1030 TTTGGCTTCAGCGCTTCATTCCTTTGTCAATCCTTTTGTATTCATTGTGTACAG 1089
QY 364 ArgPheGlnIysAlaPheLeuValIleLeuProValArgArgIleSerThrPro--Pro 382
Db 1090 CGCTTTCAAAAGGCTTTCTGAAATATTTTGTATATAAAAGCAACCTTCACATACAA 1149
QY 383 HisAsnArgSerIleSerThr 389
Db 1150 CACAGTCGGTCAGATCTTCT 1170

RESULT 14
AX376577 1266 bp DNA linear PAT 01-MAR-2002
LOCUS AX376577
DEFINITION Sequence 5 from Patent WO0200719.
ACCESSION AX376577
VERSION AX376577.1 GI:19170678
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Lin, D.C., Zhao, J., Chen, J.L. and Cutler, G.
AUTHORS Novel receptors
TITLE Patent: WO 0200719-A 5 03-JAN-2002;
JOURNAL Tularik Inc. (US)

FEATURES
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1. 1266
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ORIGIN
Alignment Scores:
Pred. No.: 4.02e-104 Length: 1266
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
DB: 6 Gaps: 3
US-10-626-398-10 (1-389) x AX376577 (1-1266)

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QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValIleValIleLeuAlaPheIleValaParg 43
Db 97 GTAGCTTTTGCTATATGCTAGGAAATGCTTGTCTATTTTACCTTTTGCTGAGCAAA 156
QY 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaPhePheVal 63
Db 157 AACCTTAGACATGCAAGTACTATTTTCTTAACCTGACATCTCTGCTCTTGTG 216
QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyIys 83

Db 217 GGTGATATCTCATCTCTTTGTATACCTCCACAGCGTGTTCGATGGATTTTGGAAAG 276
QY 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrIleAspValTyrAsn 103
Db 277 GAATGCTGTATATTTGGCTCACTACGATATCTGTATGACAGATCTGTATATAC 336
QY 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrIleArgAla 123
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QY 124 GlnHisSerGlyThrTyrIleAlaIleThrGlnMetValAlaIleTrpIlePheSerPhe 143
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QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGluCys 163
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QY 164 GlnProGlyPheLeuIysTyrTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db 517 GAACCTGATTTTTCGGAATGATATGATATGATATGATATGATATGATATGATATG 576
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Db 577 ATCCAGATCATCTTATGCTGCTTATTTCAACATGATATATTTATGAGCGTGGAAAGCGT 636
QY 204 GlnIysLeuSerTyrGlyLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 637 GATCATCTCATGATGAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 693
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Db 1174 CACAGTCGGTCAGATCTTCT 1194

RESULT 15
AX301229 1300 bp DNA linear PAT 30-NOV-2001
LOCUS AX301229
DEFINITION Sequence 1 from Patent WO0185793.
ACCESSION AX301229
VERSION AX301229.1 GI:17382320
KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1
 AUTHORS Lind, P., Sejitz, T., Vogel, G. and Wood, L.S.
 TITLE G protein-coupled receptors
 JOURNAL Patent: WO 0185793-A 1 15-NOV-2001;
 PHARMACIA & UPJOHN COMPANY (US)
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 Alignment Scores: 4,16e-104 Length: 1300
 Pred. No.: 1308.50 Matches: 252
 Score: 77.52% Conservative: 48
 Percent Similarity: 65.12% Mismatches: 84
 Best Local Similarity: 64.27% Indels: 3
 Query Match: 6 Gaps: 3
 DB: 6
 US-10-626-398-10 (1-389) x AX301229 (1-1300)
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 QY 24 LeuAlaIleAlaIleMetLeuGlyAenValValIleLeuAlaPheIleValAspArg 43
 DB 113 GTAGCTTTGCTATATAGCTAGAAATGCTTGTCATTTAGCTTTGTCGTGGCAAA 172
 QY 44 AenLeuArgHisArgSerSerThrPheLeuAenLeuAlaIleAlaPhePheVal 63
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 QY 64 GIAlaIleAlaIleProLeuThrIleProSerSerLeuThrTyrrTrpHisSerGly 83
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 QY 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
 DB 413 CAACATACCTGGGGCTCTGAAGATGTACTCTGATGTGGCCCTTGGGCTGGCCCTTC 472
 QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTyrGlnAsnSerThrGlnCys 163
 DB 473 TTAGTGAATGGCCAAATGATTTCAATTCAAGACTTGGAGAGATGAAGTAGATGT 532
 QY 164 GluProGlyPheLeuLysTyrTrpPheAlaLeuProThrSerLeuGlnPheLeu 183
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 QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
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QY 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
 DB 770 GTTCTGATCCTTTCATTCAGAGAGACAGAGAAAGATGCTATGTTTCCCTCA 829
 QY 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
 DB 830 AGAACCAAGATGAATAGCAATACATTCCTCCAAATGGGTTCTTCCCAATCAGAT 889
 QY 284 SerLeuAlaLeuGlnArgGlnHisIleGlnLeuPheArgAlaArgLysLeuAlaLys 303
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 QY 383 HisAsnArgSerIleSerThr 389
 DB 1190 CACAGTCGTCAGTATCTTCT 1210

Search completed: August 5, 2005, 21:57:04
 Job time : 4479 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2005, 17:49:01 ; Search time 573 Seconds
(without alignments)
4018.812 Million cell updates/sec

Title: US-10-626-398-10
Perfect score: 2036
Sequence: 1 MANNSTALTSIKISLTLF.....LKLIPVRQSTPPHNSIST 369

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 segs, 295870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q/cgn2.1/USPTO.epool_p/US10626398/tunat_02082005.155807_2905/app.query.fasta_1.583
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-LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=bl0sum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -ALIGN=15
-MODE=LOOCL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10626398.QCEN_1_1_709.@runat_02082005.155807_2905 -NCPUB=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: N_Geneseq.16Dec04:*
2: geneseqn19808:*
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5: geneseqn20018:*
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13: geneseqn20098:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2025	99.5	1170	6	AA170983	Guinea pig
2	1308.5	64.3	1170	3	AA055126	Human H4
3	1308.5	64.3	1173	3	AAA46023	Human G P
4	1308.5	64.3	1173	3	AA01124	Human ORP
5	1308.5	64.3	1173	4	AA033203	Human GPC

6	1308.5	64.3	1173	5	AAH24007	Human G P
7	1308.5	64.3	1173	6	ABZ80663	Human his
8	1308.5	64.3	1173	6	AB078739	Nucleotid
9	1308.5	64.3	1173	6	AA170980	Human his
10	1308.5	64.3	1173	6	AA167750	Human his
11	1308.5	64.3	1173	8	ACA93262	Human cdn
12	1308.5	64.3	1173	10	ADG98759	Human cdn
13	1308.5	64.3	1173	10	AB557063	Human ORP
14	1308.5	64.3	1173	11	AD126922	Human end
15	1308.5	64.3	1173	12	AD086374	Human end
16	1308.5	64.3	1173	12	AD088375	Novel hum
17	1308.5	64.3	1173	12	ADP20167	Human G P
18	1308.5	64.3	1173	12	ADQ75073	Human CDN
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20	1308.5	64.3	1300	6	ABA02486	Human G P
21	1308.5	64.3	1312	4	AAH47911	Human G P
22	1308.5	64.3	3689	8	ABZ42573	Human his
23	1308.5	64.3	3689	12	AD005719	Human his
24	1308.5	64.3	3689	12	AD029967	Human GPC
25	1306.5	64.2	1227	4	AA166009	Human GPR
26	1306.5	64.2	1265	6	AA598078	Human DNA
27	1306.5	64.2	1265	6	AA055125	Human H4
28	1244	61.1	1176	6	AA170981	Mouse his
29	1244	61.1	1538	12	AD030257	Mouse GPC
30	1235.5	60.7	1176	6	AA170982	Rat hista
31	1166	57.3	1166	9	AA055124	Human H4
32	1048.5	51.5	1103	9	AA055123	Human H4
33	694.5	34.1	1239	2	AA084570	G-protein
34	694.5	34.1	1239	3	AA070639	Rat G-pro
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36	693.5	34.1	2700	2	AA044571	G-protein
37	689.5	33.9	1334	2	AAH44573	Human mus
38	689.5	33.9	1335	2	AA028862	Human MAC
39	689.5	33.9	1335	3	AA09062	Human his
40	689.5	33.9	1335	4	AA062366	CDNA enco
41	689.5	33.9	1335	9	ACC59395	Human his
42	689.5	33.9	1335	10	ADD22861	Human his
43	689.5	33.9	1335	13	AD031457	Human his
44	689.5	33.9	1338	12	AD029966	Human GPC
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ALIGNMENTS

RESULT 1	AA170983	
ID	AA170983	standard; cDNA; 1170 BP.
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AC	AA170983;	
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DT	18-MAR-2002	(first entry)
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DE	Guinea pig histamine H4 receptor cDNA.	
XX		
KW	Histamine H4 receptor; guinea pig; antiallergenic; antiinflammatory; cardiact; circulatory; antidiabetic; laxative;	
KW	diagnosis; gene therapy; ss.	
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OS	Cavia porcellus.	
XX		
PN	W0200192485-A1.	
XX		
PD	06-DEC-2001.	
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PF	22-FEB-2001; 2001WO-US005914.	
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PR	31-MAY-2000; 2000US-0208260P.	
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PA	(ORTH) ORTHO-MCNEIL PHARM INC.	
XX		
PI	Lovenberg T, Liu C;	
XX		
DR	WPI; 2002-114339/15.	

DR P-PSDB; AAM50567.

XX New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.

XX Claim 4, Fig 6B; 92pp; English.

XX The present sequence is that of a cDNA clone encoding guinea pig
CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone
CC marrow cDNA library. It shows 75.6% homology to the human H4 receptor
CC coding region. The invention provides mammalian (human, mouse, rat and
CC guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-
CC 83) and polypeptides (see AAM50564-67). The nucleic acids have been
CC expressed in recombinant host cells that produce active recombinant
CC protein. The pharmacology of known histamine ligands is demonstrated.
CC Mammalian histamine H4 receptor may be used in gene therapy for the
CC treatment of diseases where it is beneficial to elevate mammalian
CC histamine H4 receptor activity. Recombinant protein is useful for
CC identifying modulators of the mammalian histamine H4 receptor. Such
CC modulators may be useful for diagnosing, treating or preventing asthma,
CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-
CC insulin dependent diabetes mellitus, hyperglycemia, constipation,
CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity

XX Sequence 1170 BP; 301 A; 286 C; 221 G; 362 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,14e-189 Length: 1170
Score: 2025.00 Matches: 388
Percent Similarity: 99.74% Conservative: 0
Best Local Similarity: 99.74% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: Gaps: 0

US-10-626-398-10 (1-389) x AAI70983 (1-1170)

QY 1 MetLeuAlaAsnAsnSerThrIleAlaLeuThrSerIleLeuSeriLeuThrPheLeu 20
Db 1 ATGTGGCAAAATTAACAGTACATCCCTTAACATCAATTAATTTCTTGACATTTTAA 60
QY 21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValAlaIleLeuAlaPheLeu 40
Db 61 ATGCTTTACTAGCATATTGCTTAATTAATGTTAGGCAATGCTGGTCAATTTTACCTTTTAT 120
QY 41 ValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAsp 60
Db 121 GTGGACAGAAATCTTAGCATGGAATTAATTTCTTTTCTTAACCTGGCCATTGCAAGC 180
QY 61 PhePheValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80
Db 181 TTCTTTGTGGGTGCAATTCATTCCTCTGTCATATACCTTCCCTGCTGACTTACGAGACT 240
QY 81 SerGlyValGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSer 100
Db 241 TCTGAAAGCAAGCTTGATATTTTGGCCATTAAGTACTTCTTTTATGACAGACACT 300
QY 101 ValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrp 120
Db 301 GTGTATATATTTGCTCTCATCAGTACGATCCCTACGATCGTCAATGCCGTGTGG 360
QY 121 TyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIle 140
Db 361 TATAAGCTCAGACACTGCTGACCTGAAATTTGCTACTCAGATGCTGCTTTGGATA 420
QY 141 PheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThr 160
Db 421 TTCTCTTCATGACAAATGGCCGAGATTCGATTTTCAGACTCTTGGCAGAAATGCACT 480
QY 161 ThrGlnCysGluProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuLeu 180
Db 481 ACAGATGTGAACCTGGATTTTAAAGGTGTACTTGTCTCTCCCTACATCATTAATTG 540

QY 181 GluPheLeuIleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeu 200
Db 541 GAATTCCTGATCCCATCTTGTATAGTCTTATTACAGGCCCATATTATTCAGAGCCGTG 600
QY 201 TrpLysArgGlyLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSer 220
Db 601 TGGAGCGAGAAACCTGAGCAGGTCGACCCGACCTGTATCTCCCTGACATCTTCC 660
QY 221 SerSerAspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAla 240
Db 661 AGCATGACACAGACATCTCTGACAGACAGACCCGATTCAGAGGCACTTGCACGCA 720
QY 241 ArgLysGlnThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeu 260
Db 721 CGAAAGAAACAACGCTCTTGTGTTCAAGCAAGTCACGGAGAAAGCAGTCTCTTG 780
QY 261 ProSerIleArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSer 280
Db 781 TTTTCATTAAGAGCTTACAAAGACGCAATGTGATCGGTTCCAAATAGGCTTCTCTCC 840
QY 281 HisSerAspSerLeuAlaLeuGlnGlnArgGlnHisIleGlnLeuPheArgAlaArgLys 300
Db 841 CACTCAGATTCCTTGCTGCTCTTACGAAAGGAAACATATCGAATTTTACAGCCAGAAA 900
QY 301 LeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSer 320
Db 901 TTAGCCAAAGTACATGGCCATCTTACATCTTTCAGACTTTTGGCATTTGGGCTCATTCA 960
QY 321 LeuThrTrpValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyr 340
Db 961 CTGACTACAGTATCTTACTCATATTTTCTTGAAAGAACTTGACTTAATCAACTGGTAC 1020
QY 341 HisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeu 360
Db 1021 CATACGCTTTTGGCTGCTCAGTGGTCAATTCCTTTGTTATCCCTTTTGTATCATTTG 1080
QY 361 CysHisLysArgPheGlnLysAlaPheLeuLysIleLeuProValAlaArgGlnSerThr 380
Db 1081 TGTCACAAAACGTTTTCAGAAAGGCTTTCCTGAAATATCTTCTGTGAGAGCAATCCAG 1140
QY 381 ProProHisAsnArgSerIleSerThr 389
Db 1141 CCACCACAAACCGCTCAATATCCACT 1167

RESULT 2
AADS5126
ID AADS5126 standard; DNA; 1170 BP.
XX AADS5126;
AC AADS5126;
XX 07-AUG-2003 (first entry)
DT Human H4 receptor wild-type DNA #2.
XX
DE
XX Human, H4; histamine receptor; inflammatory bowel disease; psoriasis;
KW atopic dermatitis; stroke; myocardial infarction; migraine; allergy;
KW chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;
KW rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;
KW asthma; receptor; gene; ds.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH 1. 1170
FT CDS
FT /tag= a
FT /product= "Human H4 protein"
FT /note= "CDS does not include stop codon"
FT /partial
XX
XX WO2003020907-A2.
XX
XX 13-MAR-2003.


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PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123944P.
PR 12-MAR-1999; 99US-0123945P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123948P.
PR 12-MAR-1999; 99US-0123949P.
PR 12-MAR-1999; 99US-0123951P.
PR 12-MAR-1999; 99US-0123951P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 28-MAY-1999; 99US-0137567P.
PR 29-JUN-1999; 99US-0141448P.
PR 27-AUG-1999; 99US-0151114P.
PR 03-SEP-1999; 99US-0152524P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156633P.
PR 29-SEP-1999; 99US-0156634P.
PR 29-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
PR 12-OCT-1999; 99US-00417044.
PA (AREN-) ARENA PHARM INC.
XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT,
PI Gore M, Llaw CM, Llin I, Lowitz K, White C;
DR WPI: 2000-117986/27.
XX P-PSDB; AAB02831.
XX Non-endogenous, human G protein-coupled receptors for screening receptor,
PT inverse or partial agonists useful as therapeutic agents.
XX Example 1; Page 88-89; 187pp; English.
XX The present invention describes transmembrane receptors, preferably human
CC G protein coupled receptors (GPCR), for which the endogenous ligand is
CC unknown (orphan GPCR receptors). More specifically the present invention
CC relates to non-endogenous, constitutively activated versions of a human
CC GPCR. These non-endogenous human GPCRs can be useful for the direct
CC identification of candidate compounds as receptor agonists, inverse
CC agonists or partial agonists for use as pharmaceutical agents. AAB0017
CC to AAB0126 and AAB02825 to AAB02859 represent sequences used in the
CC exemplification of the present invention
XX SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 8,88e-119 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
DB: 3 Gaps: 3
US-10-626-398-10 (1-389) x AAA46023 (1-1173)
QY 5 AenSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCAACAATCAATTATTCACCTAGCACTCGGTACTTTCAGATTTCCTTATGTCCTTA 72
QY 24 LeuAlaIleAlaIleLeuLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTGCTATATGCTAGGAATGCTTGGTCATTTCCTTTGCTTGGTGACAAA 132
QY 44 AenLeuArgHisArgSerAntyrPhePheLeuAsnLeuAlaIleAlaAspPhePheVal 63
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Db 123 AACCTTAGACATCGAAGTAGTATTTTCTTAACTGGCCATCTGACTTCCTTGTG 192
QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerglyAs 83
Db 123 GGTGTGATCTTCATTCCTTTTACATCCCTCACACGCTGTTGATGGATTTTGGAAAG 252
QY 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
Db 253 GAAATCTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCATCTGTATATAAC 312
QY 104 IleValIleuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123
Db 313 ATGTGCTTCATCAGCTATGATCGATACCTGCTCAGCTCAAAAGCTGTGCTTATAGAACT 372
QY 124 GlnHisSerglyThrTrpIleAlaThrGlnMetValAlaValTrpIlePheSerphe 143
Db 373 CAACATACCTGGGCTTGAAGATTCTTCTGATGCGGCCGTTTGGCTGCTGCCTTC 432
QY 144 MetThrAsnglyPrometIleLeuIleSerAspSertirpGlnAsnSerThrTrpGlyCys 163
Db 433 TTAGTGAATGGGCCAATGATTCATGTTCAAGTCTTGAAGATGAAGTAGTGAATGT 492
QY 164 GluProGlyPheLeuLeuLysTrpTyrPheAlaLeuProThrSerLeuGluPheLeu 183
Db 493 GAACTGGATTTTTCGGAATGTACATCTTGCCATCACATTCATTCGGAATTCGTG 552
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
Db 553 ATCCAGATCATCTTATGCTGCTTATTTCAACATGAATATTTATGAGCTCTGGAAGCT 612
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGGTGCAAGGCCATCTGACTGACTGCT---GTCCTTCCAACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArglySgu 243
Db 670 TGTGACACTCATTCAGAGTAGACTATCTTCAAGAAATCTTTCGACATGACAGAA 729
QY 244 ThrThrAlaSerLeuGlySerAspLysSerArgTyrGlySerSerLeuLeuProSerIle 263
Db 730 GTTCCTGATCTTCATTCATTCAGAGACAGAGAGAAAGTAGTCTCATGTTTCTCTCA 789
QY 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATGAAATGCAATATGATTCCTTCAAAAGGGTCTCTCCCAATCAGAT 849
QY 284 SerLeuAlaLeuGlnArgGlnHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
Db 850 TCTGTAGCTCTTCACCAAGGAAACATGTGAATGCTTAGAGCCAGGATTTAGCCAAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
Db 910 TCACGTGGCATTCCTTCAGGGGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969
QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTyrTrpHisThrAla 343
Db 970 ATGTGCTTCATTTATTTCCACCAAGCAGGCTCTTAATCATGTTGGATATGAATGCA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
Db 1030 TTTTGCTTCAGTGGTCAATTCCTTGTGCAATCTCTTGTATCATGTGTGTCACAAAG 1089
QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382
Db 1090 CGCTTTCAAAAGCTTCTTGAATAATTTGTATAAAAGCAACCTCTACATCAGACAA 1149
QY 383 HisAsnArgSerIleSerThr 389
Db 1150 CACAGTCGCTCAGTATCTTCT 1170
RESULT 4
AAB01124 standard; cDNA, 1173 BP.
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XX AAD01124;
 XX 02-NOV-2000 (first entry)
 XX Human orphan G protein-coupled receptor hrup7 cDNA.
 XX Human: orphan G protein-coupled receptor; GPCR; hrup7; drug screening;
 XX transmembrane receptor; signal cascade; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 1..1173
 FT /*tag= a
 FT /product= "hrup7"
 FT /note= "Human orphan G protein-coupled receptor"
 FT
 XX MO200031258-A2.
 XX 02-JUN-2000.
 XX 13-OCT-1999; 99MO-US023687.
 XX 20-NOV-1998; 98US-0109213P.
 XX 16-FEB-1999; 99US-0120416P.
 XX 26-FEB-1999; 99US-0121852P.
 XX 12-MAR-1999; 99US-0123946P.
 XX 12-MAR-1999; 99US-0123949P.
 XX 28-MAY-1999; 99US-0136436P.
 XX 28-MAY-1999; 99US-0136437P.
 XX 28-MAY-1999; 99US-0136439P.
 XX 28-MAY-1999; 99US-0136567P.
 XX 28-MAY-1999; 99US-0137127P.
 XX 28-MAY-1999; 99US-0137131P.
 XX 29-JUN-1999; 99US-0141448P.
 XX 29-SEP-1999; 99US-0156555P.
 XX 29-SEP-1999; 99US-0156633P.
 XX 29-SEP-1999; 99US-0156634P.
 XX 29-SEP-1999; 99US-0156635P.
 XX 01-OCT-1999; 99US-0157280P.
 XX 01-OCT-1999; 99US-0157281P.
 XX 01-OCT-1999; 99US-0157282P.
 XX 01-OCT-1999; 99US-0157293P.
 XX 01-OCT-1999; 99US-0157294P.
 XX 12-OCT-1999; 99US-00416760.
 XX 12-OCT-1999; 99US-00417044.
 XX (AREN-) ARENA PHARM INC.
 XX
 PI Chen R, Dang HT, Liaw CW, Lin I;
 XX WPI, 2000-40068/34.
 DR P-PSDB; AAY71297.
 XX
 PT Novel human orphan G protein-coupled receptors and the encoding cDNAs for
 PT use in the identification of G protein-coupled receptor agonists.
 XX
 XX Claim 25; Page 59; 102pp; English.
 XX
 XX The present sequence is a cDNA encoding hrup7, an endogenous human orphan
 XX G protein-coupled receptor (GPCR). The full length hrup7 cDNA was cloned
 XX by RT-PCR using human peripheral leukocyte cDNA as template. The orphan
 XX GPCR of the invention, like all GPCRs has seven transmembrane alpha
 XX helices with an extracellular N-terminus and an intracellular C-terminus.
 XX However, no endogenous ligands has yet been identified for the proteins
 XX of the invention. The orphan GPCRs may be used in the identification of
 XX their endogenous ligands, and to screen potential GPCR agonists and
 XX antagonists for use as pharmaceutical agents. The proteins may also be
 XX used in the study of GPCR-mediated signalling cascades, and to elucidate
 XX their precise role in normal and diseased human conditions. Nucleic acid
 XX encoding human orphan GPCRs may be used for tissue localisation
 XX expression analysis to provide information about their function in

CC healthy and pathological states
 XX SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8,88e-119 Length: 1173
 Score: 1308.50 Matches: 252
 Percent Similarity: 77.52% Conservative: 48
 Best Local Similarity: 65.12% Mismatches: 84
 Query Match: 64.27% Indels: 3
 DB: 3 Gaps: 3
 US-10-626-398-10 (1-389) x AAD01124 (1-1173)
 QY 5 AsnSerThrIleAlaLeuThr---SerIleValIleSerIleuThrPheLeuMetSerIleu 23
 DB 13 AATAGACAACTCAATTATTCATCTAGACACTCGGTTACTTACATTTTAAAGTCTTAA 72
 QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValIleValIleLeuAlaPheIleValAspArg 43
 DB 73 GTAGCTTTTGTCTTAATGCTAGGAAATGCTTGGTCACTTTTGTGTGACAA 132
 QY 44 AsnLeuArgHisArgSerAsnIlyrPhePheLeuAsnLeuAlaIleAlaPhePheVal 63
 DB 133 AACCTTAGACATGGAAGTAGTATTTTCTTAACCTTGCCATCTTGACTCTTGTG 192
 QY 64 GlyAlaIleAlaIleProLeuIlyrIleProSerSerIleuThrIlyrIlyrSerGlyIys 83
 DB 193 GGTGTATCTCCATCTCTTGTATCATCCACACGCTGTGCAATGGATTTTGGAAAG 252
 QY 84 GluAlaCysValPheThrPheIleuIleThrAspIlyrLeuIleuIlyrIleAsnValIlyrAsn 103
 DB 253 GAAATCTGTATTTTGGCTCACTAGTACTGATCTGTATGTACAGCATCTGTATTAAC 312
 QY 104 IleValIleuIleSerIlyrPhePheValIlyrGlnSerValSerAsnAlaValIlyrArgAla 123
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 DB 373 CAACATACCTGGGCTCTGGAAGATGTACTGTATGATGCGCTGGGCTGGCCCTTC 432
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 QY 164 GluProGlyPheLeuIlyrIlyrIlyrPheAlaIleuProThrSerLeuLeuGluPheLeu 183
 DB 493 GAACCTGGAATTTTTCGGAATGATGATCATCTTGCATCATCTTCTGGAATTCGTG 552
 QY 184 IleProIleLeuLeuValAlaIlyrPheSerAlaHisIleIlyrIlyrSerIleuIlyrGly 203
 DB 553 ATCCAGATCATCTTATCGCTTATTTTCAACATGAATATTTATTTGAGCCGTGGAAGCGT 612
 QY 204 GluIlyrLeuSerArgCysIleuSerHisProValIleProSerAspSerSerSerAsp 223
 DB 613 GATCATCTCAATGATGGTCCAAAGCATCTTGACATGACGCT---GTCCTTCAACATC 669
 QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgIlyrGly 243
 DB 670 TGTGACACATCATTTAGAGGTAGATCATCTTCAAGAGATCTCTTCTGATGACAGAA 729
 QY 244 ThrThrAlaSerIleuGlySerAspIlyrSerArgIlyrIlyrSerSerIleuProSerIle 263
 DB 730 GTTCTGCACTCTTTCATTCAGAGACAGAGAGAGAAAGTAGTCTCATGTTTCTCTCA 789
 QY 264 ArgAlaIlyrIlyrAsnSerAsnValIleAlaSerIlyrMetGlyPheLeuSerHisSerAsp 283
 DB 790 AGAACCAAGATGAATGCAATACATTTCTTCCAAATGGCTTCTTCCCAATGAGAT 849
 QY 284 SerLeuAlaLeuGlnIlyrGlnIlyrIleGluLeuPheArgAlaArgIlyrIleuAlaIlyr 303
 DB 850 TGTGTAGCTCTTACCAAGGAAAGGAAATGTTGAATGCTTAGAGCCAGAGATTAGCCAAG 909

QY	304	SeftiLlAlaIleLeuLeuAlaAlaIleCysTTPAlaProTySerLeuThr	323
Db	910	TCACGGCCATTCCTTAGGGGCTTTTGGTGGTCTGGCCATATCTCTGTACCA	969
QY	324	VallIeTySerPhePheProGluArgAnLeuThrLySserThrTTPTyHieThAla	343
Db	970	ATTCGCTTTTCACTTTTATTTCCCTCACACAGGCTCTMAATCATGTTGGTATAGAAATTGCA	1029
QY	344	PheTTPLeuGlnTTPPheAnSerpheValaAnProPheLeuTyPProLeuCyHisIlyS	363
Db	1030	TTTTGGCTTCAGTGGTTCATCTCTTGCAATCCTCTTTGTGTATCCATTTGTGCACAG	1089
QY	364	ArgPheGlnIlyAlaPheLeuIlyLeuProValaArgGlnSerThrPro---Pro	382
Db	1090	CGCTTTCAAAGGCTTCTTGAAAAATTTGTATAAAAAGCAACCTTACATACACA	1149
QY	383	HisAnArgSerIleSerThr	389
Db	1150	CACAGTCGGTCAGTATCTTCT	1170
RESULT 5			
AAFB3203			
ID	AAFB3203	standard; cDNA; 1173 BP.	
XX	AC	AAFB3203;	
XX	AC	AAFB3203;	
DE	09-JUL-2001	(first entry)	
XX	XX	Human GPCR-like polypeptide, PFI-013 encoding cDNA.	
XX	XX	G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;	
KW	XX	antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;	
KW	XX	osteopathic; neuroprotective; nootropic; dermatological; gynecological;	
KW	XX	signal transduction; ss.	
XX	OS	Homo sapiens.	
XX	XX		
PH	Key	Location/Qualifiers	
FT	CDS	1..1173	
FT		/*tag= a	
FT		/product= "PFI-013"	
XX	PN	EP1096009-A1.	
XX	PD	02-MAY-2001.	
XX	PF	24-OCT-2000; 2000EP-00309364.	
XX	PR	29-OCT-1999; 99GB-00025641.	
PR	PR	20-APR-2000; 2000GB-00009973.	
XX	PA	(PFI2) PFIZER LTD.	
XX	PA	(PFI2) PFIZER INC.	
XX	PI	Peter B. O'reilly MA;	
XX	DR	MP1: 2001-109854/33.	
XX	DR	P-PSDB; AAB62445.	
PT	PT	New G-protein coupled receptor-like polypeptide, polynucleotide for	
PT	PT	screening drug candidates for treating diseases associated with signal	
XX	XX	transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.	
PS	PS	Claim 1; Page 43; 66pp; English.	
XX	XX		
CC	CC	This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor	
CC	CC	(GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be	
CC	CC	expressed by standard recombinant methodology. Antibodies and modulators	
CC	CC	of PFI-013 are useful in the manufacture of a medicament for treating	
CC	CC	allergic disorder, including extrinsic asthma, immunological disorders,	
CC	CC	such as intrinsic asthma, vasculitic granulomatous disease, interstitial	
CC	CC	and other pulmonary disease, including chronic obstructive pulmonary	

CC	diseases (COOP), infectious, inflammatory disease, such as inflammatory
CC	bowel disease and neoplastic and myeloproliferative diseases. They are
CC	also useful for treating obesity, diabetes, metabolic, neurological
CC	diseases, psychotherapeutics, urogenital diseases, reproduction and sexual
CC	medicine, inflammation, cancer, tissue repair, dermatology, photogelatin
CC	skin pigmentation, osteoporosis, cardiovascular, gastrointestinal
CC	diseases, allergy and respiratory disease, sensory organ disorders, sleep
CC	disorders and hair loss. The P1-103 protein and nucleic acid are useful
CC	in the diagnosis and treatment of the above conditions and also for
CC	screening drug candidates for the treatment of diseases associated with
CC	signal transduction. The antibodies are also useful for enrichment of
CC	eosinophils from mammalian, especially human blood and for detecting the
CC	protein in biological samples
XX	
80	Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	8,886-119 Length: 1173
Score:	1308.50 Matches: 252
Percent Similarity:	77.52% Conservative: 48
Best Local Similarity:	65.12% Mismatches: 84
Query Match:	64.27% Indels: 3
DB:	4 Gaps: 3
US-10-626-398-10 (1-389) x AAF83203 (1-1173)	
QY	5 AaNSerTThlAlaLeuThr---SerIleYsIleSerLeuThrPheLeuMetSerLeu 23
DB	13 AATACACAAATCAATTTATCACTAAGCACTCGGTACTTTAGCATTTTATATGCTCTTA 72
QY	24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValaAArg 43
DB	73 GTACCTTTGGCTAAATAGCTAGGAATCGTTGGTCATTTTAGCTTTGGTGGCAAA 132
QY	44 AsnLeuATGHisARSerAsnTrpPhePheLeuAsnLeuAlaIleAlaAspPhePheVal 63
DB	133 AACCTTAGCACTGAAAGTAGTAGTTATTTTCTTAACCTTGACATCTGACTCTTTTG 132
QY	64 GYAlaIleAlaIleProLeuTrpIleProSerSerLeuThrTrpTrpHisSerGlyLys 83
DB	193 GGTGTGATCTCCATTCCTTTGTACATCCCTCAACAGCTGTGGAAAGGATTTTGGAAAG 252
QY	84 GlnAlaCyGValPheTrpLeuIleThrAspTrpLeuLeuCyGThrAlaSerValTrpAsn 103
DB	253 GAATATCTGTAAATTTTGGCTACTGCTACTGCTATCTGTATGTAGACACATCTGTATTAAC 312
QY	104 IleValIleuIleSerTrpAspArgTrpGlnSerValSerAsnAlaValTrpTrpArgAla 123
DB	313 ATGTGCTCATACGATCATGATGATGATACCTGTCAAGTCTCAAAAGCTGTGTTATAGAAC 372
QY	124 GlnHisSerGlyThrTrpIleIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
DB	373 CAACATACAGGGGCTCTTGAAGATTGTACTCGATGATGTCGCCGTTGGGGTGGCCCTTC 432
QY	144 MetTrpAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGlnCys 165
DB	433 TTAGGAAATGGCCAAATGATTTTACGTTTAGAGTCTTGGAAAGATGAAAGTAGTAATGT 422
QY	164 GlnProGlyPheLeuLysIleTrpTrpPheAlaLeuProThiSerLeuLeuGlnPheLeu 183
DB	493 GAACCTGGATTTTTTTCGGAATGATGATACCTTGGCATCACATCTTGGATTCGTG 552
QY	184 IleProIleLeuLeuValAlaTrpPheSerAlaHisIleTrpTrpSerLeuTrpLysArg 203
DB	553 ATCCAGATCATCTTGAAGCTTATTTCAACATGAATATTTATTTAGAGCCGTGGAAGCGT 612
QY	204 GlnLysLeuSerArgCysLeuSerHisProValIleProSerAspSerSerSerAsp 223
DB	613 CATCATCTCAGTAGAGGTGCCAAAGCATCTTGAGACTGACGTGCT---GTCTCTTCAACATC 665
QY	224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGln 243
DB	670 TGTGACACTCAATTGAGAGTAGATCATCTTCAAGAGAGATCTCTTCTTCGATGACAGAA 729

QY	244	ThrlthlAserLeuGLySerAspSerySerArgGLySerSerSerLeuLeuProSerIle	263
Db	730	GTTCCTGCATCTCTTCATTCACAGACAGACAGACAGAAAGATGATCTCATGTTCCTCA	789
QY	264	ArgAlaTryIysAasnSerAsnValIleAlaSerIysMetGIyPheLeuSerHisSerAsp	283
Db	790	AGAACCAGATGATATAGCAATATACATATGCTCCAAATAGGGTTCCTCCCAATCAGAT	849
QY	284	SerLeuAlaLeuGLnIlnArgGLnHisIleGIuLeuPheArgAlaArgIyLeuAlaIys	303
Db	850	TCGTAGCTCTTCACCAAAAGGAACAGTGAACGCTTAAAGCCAGGATTAAGCCAAAG	909
QY	304	SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProIySerLeuThrThr	323
Db	910	TCACGTGGCATCTCTTAGAGGGGTTTTCGTCTGTTCGTGGCTCCATATCTCTGTCCAC	969
QY	324	ValIleTrySerPhePheProGIuArgAsnLeuThrIySerThrTrpTryHisThrAla	343
Db	970	ATTGCTCTTCATTTATTTCTCCACAGCAACAGTCTCTTAATCAGTTGGTATAGAAATTC	1029
QY	364	ArgPheGlnIyValAlaPheLeuIyIleLeuProValArgArgGlnSerThrPro---Pro	382
Db	1090	CGCTTTCAAAAGCGCTTCTTGAAAATATTTTGATATATAAAAGCAACCTTCACATCAC	1149
QY	383	HisAsnArgSerIleSerThr	389
Db	1150	CACAGTCGGTCAGATCTTCT	1170
RESULT 6			
AAH24007	ID		
AAH24007	standard; cDNA; 1173 BP.		
AAH24007;	ID		
10-NUG-2001	(first entry)		
Human G protein-coupled receptor AXOR35 cDNA.			
AXOR35; human; G protein-coupled receptor; 7TM receptor;			
histamine H3 receptor homologue; infection; viral; bacterial; fungal;			
protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;			
bulimia; osteoporosis; asthma; allergy; urinary retention;			
acute heart failure; hypotension; hypertension; angina pectoris;			
myocardial infarction; stroke; ulcer; migraine; vomiting;			
psychotic disorder; neurological disorder; anxiety; schizophrenia;			
manic depression; bipolar disorder; depression; delirium; dementia;			
severe mental retardation; dyskinesia; Parkinson's disease;			
Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;			
macrophage; eosinophil; neutrophil; function modulation;			
autoimmune disorder; pulmonary disorder; gene therapy; vaccine;			
drug screening; signal transduction; transgenic animal; drug discovery;			
se.			
OS	Homo sapiens.		
XX			
XX	Key		
XX	FH CDS		
XX	FT 1..1173		
XX	FT /*tag= a		
XX	FT /product= "Human AXOR35"		
XX	FT /note= "G protein-coupled receptor"		
XX	FN		
XX	MO200133221-A1.		
XX	10-MAY-2001.		
XX	26-OCT-2000; 2000MO-US029461.		
XX	26-OCT-2000; 2000MO-US029461.		
XX	02-NOV-1999; 99US-00431898.		
XX	RR		

```

PR 03-FEB-2000: 2000US-00497790.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX
P1 Aubart KM, Bergsma DJ, Flitzgeraid LR, Graybill TL, Li X;
P1 Michalovich D, Morrow DM, Zhu Y,
XX
XX
DR MPI: 2001-316464/33.
DR P-PSDB; AAB373622.
XX
XX
PT Novel G-protein coupled receptor polypeptide and polynucleotide for
PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological
PT disorders and for identifying modulators useful for treating asthma.
XX
XX
PS Claim 2, Page 49-50; 54dp; English.
XX
XX
CC The invention relates to the human G protein-coupled receptor AXOR35
CC (AAB373622), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments
CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative
CC transmembrane domains and is involved in signal transduction. AXOR35 has
CC homology and structural similarity with G protein-coupled receptors such
CC as the human histamine H3 receptor. The invention also relates to
CC expression vectors and host cells comprising AXOR35 DNA, to recombinant
CC expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 protein
CC and nucleotides may be used to treat a wide variety of disorders
CC including bacterial, fungal, protozoal and viral infections, particularly
CC HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy;
CC diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;
CC urinary retention; acute heart failure; hypertension; angina;
CC psoriasis; myocardial infarction; stroke; ulcers; migraine; vomiting;
CC psychotic and neurological disorders such as anxiety, schizophrenia,
CC manic depression, depression, delirium, dementia, and severe mental
CC retardation, and dyskinesias, such as Parkinson's disease, Huntington's
CC disease or Gilles de la Tourette's syndrome. AXOR35 proteins and
CC nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and
CC antibodies may be used in screening compounds for their ability to
CC modulate AXOR35 activity or expression. Such AXOR35 modulators are
CC particularly useful for treating asthma, and inhibiting or promoting the
CC function of lymphocytes, macrophages, eosinophils or neutrophils in
CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also
CC useful for diagnosing or determining susceptibility of an individual to a
CC disease via the detection of abnormal levels of protein or mRNA, or via
CC the detection of mutations in the corresponding gene. AXOR35 proteins are
CC also useful for inducing an immunological response in a mammal against
CC the above diseases, and for antibody production. AXOR35 nucleotides are
CC also useful as diagnostic reagents, in chromosome localisation and tissue
CC expression studies, and for producing transgenic animals useful in drug
CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35
CC protein or fragments thereof, and are also useful for treating conditions
CC associated with the expression of the AXOR35 protein. The present
CC sequence represents cDNA encoding human AXOR35
XX
XX
Q2 Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
XX
XX
XX
Alignment Scores:
Pred. No.: 8, 886-119 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 84
Best Local Similarity: 65.12% Mismatches: 48
Query Match: 64.27% Indels: 3
DB: 5 Gaps: 3
US-10-626-398-10 (1-389) * AAH24007 (1-1173)
QY 5 AasnSerThrIleAlaIeuThr---SerIleYsIleSerIeuThrPheLeuMetSerIeu 23
Db 13 AATAGACAAATCAATTATCATCTAGACACTCGTGTACTTAGACATTTTATATCCTTA 72
QY 24 LeuAlaIleAlaIleIleIeuIeuIeuIeuValValValIleIeuAlaIleValAspArg 43
Db 73 GTAGCTTTTGTCTATATATGCTAGAAATGCTTTGGTCATTTTAGCTTTGTGTGTGACAAA 122

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QY 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePheVal 63
DB 133 AACCTTAGCATGAGTAGTATTATTTTCTTAACCTTGCCATCTCTGACTCTTTGTG 192
QY 64 GlValAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpHisSerGlyAs 83
DB 139 GGTGGATCTCCATTCCTTCTTGACATCCCTCACACGCTCTTGGAATGGGATTTGGAAAG 252
QY 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
DB 253 GAAATCTGTGTAATTTGGCTCACTACTGACTATCTGTATTGACAGCATCTGATATATAC 312
QY 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrAla 123
DB 313 ATGTGCTCATCAGCATATGATGATACCTGACAGTCTCAAAAGCTGTGCTTATAGAACT 372
QY 124 GlnHisSerGlyThrTrpValIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
DB 373 CACATCTCTGGGCTCTTGAGATTTGTTACTCTGATGCTGCGGTGGCTGGCGCTTC 432
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGluCys 163
DB 433 TAGAGGAATGGGCAATGATTTCTAGTTTCAGAGTCTGGAAGATGAAGTAGTAGAT 492
QY 164 GluProGlyPheLeuLeuLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
DB 493 GAACCTGGATTTTTCGGAATGATGATCCTTGCCATCACATCTTCTTGGAATTCGTG 552
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysAsp 203
DB 553 ATCCAGATATCTTACCTGCTTATTTCAACATGAAATTTATGGAGCTGTGGAAAGCT 612
QY 204 GluLysLeuSerArgCysLeuSerHisProValIleProSerAspSerSerSerAsp 223
DB 613 GATCATCTCAGTAGAGGCAAAAGCCATCTCGACGTACGTCT---GTCTTCCAACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
DB 670 TGTGGACTCATTCACAGGATGACATATCTTCAAGAGATCTCTTCTTCATCGACAGAA 729
QY 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
DB 730 GTTCTGCGATCTCTTTCATTCACAGACACAGAGAAAGATGATCTCATGTTTCTCTCA 789
QY 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGAATAGCAATACATATGCTTCAAAATGGTCTCTCCCAATCAGAT 849
QY 284 SerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
DB 850 TCTGTAGCTCTTCACCAAGGAAACATGTTGAACCTGTAGAGCCGAGGATTAGCCAAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaIleAlaPheAlaIleCysTrpAlaProTyrSerLeuThr 323
DB 910 TCACTGGCCATCTCTTACGGGCTTTTGTGCTGTGGGCTCCCATATCTCTGTTCA 969
QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343
DB 970 ATGTGCTCTTCAATTTATCTCCACAGACAGGCTCAATATCCTTTGTATCCATTTGTCA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
DB 1030 TTTTGCTTCAGTGTGTTCAATTCCTTTGTCAATCCCTTTTATCCATTTGTGTCAAG 1089
QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgIleSerThrPro---Pro 382
DB 1090 CGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAAGAACCTTACATCACAA 1149
QY 383 HisAsnArgSerIleSerThr 389
DB 1150 CACAGTCGGTCAGTATCTTCT 1170

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, RESULT 7

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ABZ80663
ID ABZ80663 standard; cDNA; 1173 BP.
XX
AC ABZ80663;
XX
DT 13-JUN-2003 (first entry)
XX
DE Human histamine receptor coding sequence.
XX
KW human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;
KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;
KW anti-migraine; cardiac; anti-rheumatic; anti-arthritic; antipsoriatic;
KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;
KW myocardial infarction; migraine; chronic obstructive pulmonary disease;
KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
KW psoriasis; receptor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1173
FT /tag=a
FT /product="Histamine receptor"
XX
PN US6204017-B1.
PD 20-MAR-2001.
XX
PF 07-OCT-1999; 99US-00414010.
XX
PR 07-OCT-1999; 99US-00414010.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Behan JX, Hedrick JA, Laz TM, Monema FJ, Morse KL, Umland SP;
PI Wang S;
XX
DR WPI; 2002-442063/47.
XX
P-PSDB; AB098629.
XX
PT New nucleic acid encoding antigenic part of human histamine receptor,
PT useful for preparing antibodies, e.g. for treating-histamine related
PT disorders.
XX
PS Example 1; Col 27-28; 19pp; English.
XX
CC This sequence represents the open reading frame for a human histamine
CC receptor (HR) designated SP9144. The sequence was isolated by searching
CC databases with the sequence of known G-coupled protein receptor (GPCR).
CC The gene is used for recombinant production of HR and for preparing
CC antibodies (Ab). These Ab are used to purify HR by immunofinity
CC chromatography, in immunosay of histamine receptor, to identify cDNA
CC clones that express the receptor, as antagonist to block binding of
CC histamine (for treating any histamine-associated disorder) and to
CC generate anti-idiotypic antibodies. Agonists and antagonists of the HR
CC protein can be used in the treatment of e.g. inflammation, asthma,
CC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,
CC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple
CC sclerosis, inflammatory bowel disease and psoriasis
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 8.88e-119 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
DB: 6 Gaps: 3
US-10-626-398-10 (1-389) x ABZ80663 (1-1173)

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QY 5 AsnSerThrIleAlaLeuThr--SerIleLysIleSerLeuThrPheLeuMetSerLeu 23

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Db      13  AATAGCACAATCATTTATCATCTAAGACATCGTGTACTTATGACTTTTATATCTCTTA 72
Qy      24  LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db      73  GTAGCTTTCTTAATAGCTAGGAAATGCTTGCTTTAGCTTTTGTGTGGACAA 132
Qy      44  AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaPhePheVal 63
Db      133  AACCTTAGACATCGAATAGTATTTTCTTACTTGGCCATCTCTGACTTCTTTGTG 192
Qy      64  GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpHisSerGly 83
Db      193  GGTGTGATCTCATCTTCTTGTACATCCCTCACACGCTGTTCGAATGGATTTTGAAG 252
Qy      84  GluAlaGlyValPheTrpLeuIleThrAspTyrLeuLeuGlySerThrAlaSerValTyrAsn 103
Db      253  GAAATCTGTATTTTGGCTCAGTACGACTATCTGTATGTACAGCATCTGTATATAC 312
Qy      104  IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTyrArgAla 123
Db      313  ATTGCTCTCATCACTATGATTCAGTACCTGCTCAATGCTGTCTTATAGACT 372
Qy      124  GluHisSerGlyThrTrpIleAlaIleThrGlnMetValAlaValTrpIlePheSerPhe 143
Db      373  CACATCTAGTGGGCTGGAAGATGTACTGTATGTTGGCCGCTTGGTGGCTGCCTTC 432
Qy      144  MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGluCys 163
Db      433  TTAGTGAATGGCCAAATGATTTAGTTTCAAGTCTTGGAAGTGAAGTGAATGT 492
Qy      164  GluProGlyPheLeuGlyValTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db      493  GAACTGGATTTTTCGAAATGATGATCTTCCATCATCATCTTGGAAATTTGTG 552
Qy      184  IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpIleArg 203
Db      553  ATCCAGTCACTTACGCTTATGCTTATTCACATGAAATTTATGAGACCTGTGGAACGT 612
Qy      204  GluLeuLeuSerArgCysLeuSerHisProValLeuProSerLeuSerSerSerSerAsp 223
Db      613  GATCATCTCAGTAGTGCCTCAAGGCATCTGAGTGTGCTCT--GTCTCTTCCAAATC 669
Qy      224  HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgGlyGlu 243
Db      670  TGTGACACTCATTCAGAGTACACTATCTTCAAGGAGATCTTTTGCATCCACAGAA 729
Qy      244  ThrThrAlaSerLeuGlySerAspIleSerArgIleGlySerSerLeuLeuProSerIle 263
Db      730  GTTCTGCAATCTTTTCAATCAGAGACAGAGAGAGAGATGTCATGTTTCTCA 789
Qy      264  ArgAlaTyrIleAsnSerAsnValIleAlaSerIleMetGlyPheLeuSerHisSerAsp 283
Db      790  AGAACCAAGATGATATACCAATGCTTCCAAATGGGTTCTTCTCCCATCAGAT 849
Qy      284  SerLeuAlaLeuGlnGlnIleArgGlyHisIleGlyLeuPheArgAlaArgIleLeuAla 303
Db      850  TCTGACTCTTCCCAAGGAGACATGTGACTTGAAGCAGAGATTAGCCAG 909
Qy      304  SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
Db      910  TCATGCGCATCTCTTAAGGGTTTGTGCTGTGCGGGCTCATTTCTCTGTACA 969
Qy      324  ValIleTyrSerPhePheProGluArgAsnLeuThrIleSerThrTrpTyrHisThrAla 343
Db      970  ATTGCTCTTCTATTATCTCTCAGCAACAGTCTTAATCAGTTGTGTAGAAATGCA 1029
Qy      344  PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisIle 363
Db      1030  TTTTGGCTTCAAGTGTCAATCTTGTGTCAATCTTTGTGTATGCCATGTGTGACAG 1089
Qy      364  ArgPheGlnIleValPheLeuIleLeuProValArgArgIleSerThrPro--Pro 382

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Db      1090  CGCTTCAAAAGCGTTCTTGGAAAATATTTGTATATAAAAGCACTTACATCACAA 1149
Qy      383  HisAsnArgSerIleSerThr 389
Db      1150  CACAGTGGTCAAGATCTTCT 1170

RESULT 8
ABQ78739
ID  ABQ78739 standard; DNA; 1173 BP.
AC  ABQ78739;
DT  05-DEC-2002 (first entry)
XX
DE  Nucleotide sequence of human histamine receptor.
XX
KW  Human; histamine receptor; receptor; inflammation; asthma; allergy;
KW  atopic dermatitis; stroke; myocardial infection; migraine;
KW  chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;
KW  multiple sclerosis; inflammatory bowel disease; psoriasis;
KW  intracellular second messenger pathway; cellular growth rate;
KW  hormone secretion; gene; 88.
XX
OS  Homo sapiens.
XX
FH  Key  Location/Qualifiers
FT  CDS  1..1173
FT      /*tag = a
FT      /product= "histamine receptor"
XX
PN  US2002098539-A1.
XX
PD  25-JUL-2002.
XX
PF  19-MAR-2001; 2001US-00812216.
XX
PR  07-OCT-1999; 99US-00414010.
XX
PA  (BEHA/) BEHAN J X.
PA  (HEDR/) HEDRICK J A.
PA  (LAZT/) LAZ T M.
PA  (MONS/) MONSMA F J.
PA  (MORS/) MORSE K L.
PA  (UMLA/) UMLAND S P.
PA  (WANG/) WANG S.
XX
PI  Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP,
PI  Wang S;
PI
DR  WPI: 2002-673827/72.
DR  P-PSDB; ABB78276.
XX
PT  Novel mammalian histamine receptor polypeptide useful for identifying
PT  agonist or antagonist for treating diseases such as inflammation, asthma,
PT  stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.
XX
PS  Example 1; Page 15-16; 21pp; English.
XX
XX
CC  The present sequence encodes a human histamine receptor. The polypeptide
CC  is useful for identifying an agonist or antagonist of a mammalian
CC  histamine receptor. It is useful as an antigen to elicit the production
CC  of antibodies. The histamine receptor polypeptide and polynucleotide are
CC  useful in the treatment and management of diseases such as inflammation,
CC  asthma, allergy, atopic dermatitis, stroke, myocardial infection,
CC  migraine, chronic obstructive pulmonary disease (COPD), rheumatoid
CC  arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.
CC  They are also useful for modulating intracellular second messenger
CC  pathway activated through histamine receptors (cyclic-AMP, calcium,
CC  inositol phosphate and mitogen activated protein (MAP) kinase), changes
CC  in cellular growth rate, secretion of hormones, receptor-stimulated Ca2+
CC  mobilization, mitogenic effects, etc
XX
SQ  Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

```

Alignment Scores:

Pred. No.:	8,88e-119	Length:	1173
Score:	1308.50	Matches:	252
Percent Similarity:	77.52%	Conservative:	48
Best Local Similarity:	65.12%	Mismatches:	84
Query Match:	64.27%	Indels:	3
	6	Gaps:	3

US-10-626-398-10 (1-389) x AB078739 (1-1173)

```

QY 5 AenSerThrIleAlaLeuThr---SerIleuYsIleSerLeuThrPheLeuMetSerLeu 23
DB 13 AATACACACATCAATTTATACACTAGACACTCGGTGATCTTAGCAATTTTATGCTTCA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAenValIleValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTGGCTATATAGCTAGAAATGCTTTGGTCACTTTTAGCTTTTGGTGACAA 132
QY 44 AenLeuAArgHisArgSerAenTyrrPhePheLeuAenLeuAlaIleAlaAspPheVal 63
DB 133 AACCTTAGACATCGAAGTAGTATTTTCTTAACCTTGCCATCTGCACTTCTTG 192
QY 64 GlyAlaIleAlaIleProLeuTyrrIleProSerSerLeuThrTyrrTrpSerGlyLys 83
DB 193 GGTGATCTCCATTCCTTTGACATCCCTCACAGCTGTCGAATGGGATTTGGAAAG 252
QY 84 GlnAlaCyValPheTrpLeuIleThrAspTyrrLeuLeuCySerThrAlaSerValTyrrAen 103
DB 253 GAAATCTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGACTGTATATAC 312
QY 104 IleValIleLeuIleSerTyrrAspArgTyrrGlnSerValSerAsnAlaValTrpTyrrAla 123
DB 313 ATGTGCTCATGAGCATATGATCGATCGATCGATCGATCGATCGATCGATCGATCGAT 372
QY 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
DB 373 CACACACTGCGGGCTTGAAGATGTTACTGTGATGCGCGGTGGGTGGCTTGC 432
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrArgLys 163
DB 433 TTAGGGAATGGGCCAATGATTTCTAGTTTCAGAGCTCTGGAAGATGAAAGTACTGAT 492
QY 164 GlnProGlyPheLeuLysIleTyrrPheAlaLeuProThrSerLeuGlnPheLeu 183
DB 493 GAACCTGGATTTTTCGGAATGATGATCGATCGATCGATCGATCGATCGATCGAT 552
QY 184 IleProIleLeuLeuValAlaTyrrPheSerAlaHisIleTyrrTrpSerLeuTrpLysArg 203
DB 553 ATCCCAAGTATCTTAGTCCCTTATTTCAACATGAATATTATTTGAGCTGTGGAAGCT 612
QY 204 GlnLysLeuSerArgCySerLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 613 GATCATCTCAGTAGAGTGCAGAAAGCCATCTTGAGTCACTGCT---CTCTCTTCCAACATC 669
QY 224 HisGlyHisSerCyArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGln 243
DB 670 TGTGACACTCATTTAGAGTAGACTACTATTCAAGGAGATCTCTTCTTCATCGACAGA 729
QY 244 ThrThrAlaSerLeuGlnYserAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
DB 730 GTTCTGCACTCTTTCATTCAGAGACACAGAGAGAAAGTAGTCTCAATGTTTCTCA 789
QY 264 ArgAlaTyrrLysAsnSerAenValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGTCTCTTCCCAATCGAT 849
QY 284 SerLeuAlaLeuGlnArgGlnArgHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
DB 850 TCTGTAGCTCTTACCAAGGAGAACTGTTGAATGCTTAGAGCCAGAGATTAAGCAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCySerThrAlaProTyrrSerLeuThrTrp 323
  
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DB 910 TCAGTGCCCATCTCTTAGAGGGTTTTCGCTTTGCTGGGCTCCAAATTCCTGTAC 969
QY 324 ValIleTyrrSerPhePheProGlnArgAenLeuThrLysSerThrTrpTyrrHisThrAla 343
DB 970 ATGTGCTTTCACTTTATTTATTCACAGCAACAGTCTCTMAATCAGTTTGGTATGAATGCA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAenProPheLeuTyrrProLeuCyHisLys 363
DB 1030 TTTTGGCTTCAAGTGGTCAATCTTTGTCAATCTCTTTTGTATTCATTTAGTGCACAA 1089
QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382
DB 1090 GCGTTTCAAAAGGCTTTCTTGAAATATTTGTATTAATAAGCACTCTACACACAA 1149
QY 383 HisAenArgSerIleSerThr 389
DB 1150 CACAGTCGATAGTATCTTCT 1170
  
```

RESULT 9
AA170980
ID AA170980 standard; cDNA; 1173 BP.
XX
AC AA170980;
XX
XX 18-MAR-2002 (first entry)
DT
XX
DE Human histamine H4 receptor cDNA.
XX
KW Histamine H4 receptor; human; antiaesthetic; anti-allergenic;
KW antinflammatory; cardiac; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy; ss.
OS Homo sapiens.
PN MO200192485-A1.
XX
PD 06-DEC-2001.
XX
PF 22-FEB-2001; 2001WO-US005914.
XX
PR 31-MAY-2000; 2000US-0208260P.
XX
PA (ORTHO) ORTHO-MCNEIL PHARM INC.
XX
PI Lovenberg T, Liu C;
XX
DR WPI: 2002-11439/15.
XX
PS P-PSDB: AAM50564.
XX
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
XX beneficial to elevate mammalian histamine H4 receptor activity.
XX
PS Claim 4; Fig 1; 92pp; English.
XX
CC The present sequence is that of cDNA clone pH4R encoding a human
CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone
CC marrow cDNA library. The invention provides mammalian (human, mouse, rat
CC and guinea pig) histamine H4 receptor nucleic acid molecules (see
CC AA170980-83) and polypeptides (see AAM50564-67). The nucleic acids have
CC been expressed in recombinant host cells that produce active recombinant
CC protein. The pharmacology of known histamine ligands is demonstrated.
CC Mammalian histamine H4 receptor may be used in gene therapy for the
CC treatment of diseases where it is beneficial to elevate mammalian
CC histamine H4 receptor activity. Recombinant protein is useful for
CC identifying modulators of the human histamine H4 receptor. Such
CC modulators may be useful for diagnosing, treating or preventing asthma,
CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-
CC insulin dependent diabetes mellitus, hyperglycemia, constipation,
CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8,88e-119 Length: 1173
 Score: 1308.50 Matches: 252
 Percent Similarity: 77.52% Conservative: 48
 Best Local Similarity: 65.12% Mismatches: 84
 Query Match: 64.27% Indels: 3
 DB: 6 Gaps: 3

US-10-626-398-10 (1-389) x AA170980 (1-1173)

QY 5 AasnSerThrIleAlaLeuThr---SerIleValIleSerIleuThrPheLeuMetSerLeu 23
 DB 13 AATAGACACATCAATTTATTCACACACACGCTGTTACTTACCTTATGATGCTTA 72
 QY 24 LeuAlaIleAlaIleuLeuGlyAsnValValIleLeuAlaPheIleValaParg 43
 DB 73 GTAGCTTTGCTTAATAGCTAGGAAATGCTTGCTCATTTTACCTTTGGGGACAA 132
 QY 44 AasnLeuArgHisArgSerAsnIlePhePheLeuAsnLeuAlaIleAlaPhePheVal 63
 DB 133 AACCTTAGACATGAGAGTACTTATTTTCTTAACCTGGCCATCTCTGACTCTTG 192
 QY 64 GlyAlaIleAlaIleProLeuIleProSerSerLeuThrIleProSerGlyIle 83
 DB 193 GGTGTGATCTCCATCTCTTGTACATCCCTCACACGCTGTTGAATGGAGTTTGA 252
 QY 84 GluAlaCysValPheThrLeuIleThrAspTyrLeuLeuCysThrAlaSerValIle 103
 DB 253 GAATGTGTATTTGGCTGACTGACTGACTGACTGACTGACTGACTGACTGACTG 312
 QY 104 IleValIleuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrIle 123
 DB 313 ATTGCTCATGACGCTATGATGATGATGATGATGATGATGATGATGATGATG 372
 QY 124 GlnHisSerGlyThrTyrIleAlaIleAlaIleMetValAlaValIlePheSer 143
 DB 373 CAACATACGAGGGGCTTTGAAGATTGTACTCTGATGATGATGATGATGATG 432
 QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTyrGlnAsnSerThrIle 163
 DB 433 TTAGTGAATGGGCAATGATTTAGTTTCAAGCTTTGGAAGATGAAGTATGA 492
 QY 164 GluProGlyPheLeuIleSerTyrIlePheAlaLeuProThrSerLeuGluPhe 183
 DB 493 GAACCTGGAATTTTTCGGAATGATGATGATGATGATGATGATGATGATG 552
 QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrIleProSer 203
 DB 553 ATCCCAAGTACTTATGCTGCTTATTTCAACATGATATTATTAGAGCGTGA 612
 QY 204 GluValLeuSerArgCysLeuSerHisProValLeuProSerAspSerSer 223
 DB 613 GATCATCTAGTAGGAGCCAAAGCCATCTCGACATGCT---GTCTCTTCA 669
 QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrIleProAla 243
 DB 670 TGTGGACACTCATTCAGAGTACATATCTTCAAGAGATCTTTCTGATGACA 729
 QY 244 ThrThrAlaSerLeuGlySerAspIleSerArgIleGlySerSerLeuLeu 263
 DB 730 GTTCTCGCATCTTTCATTCAGAGACAGAGAGAGAGAGAGAGAGAGAG 789
 QY 264 ArgAlaTyrIleAsnSerAsnValIleAlaSerIleMetGlyPheLeuSerHis 283
 DB 790 AGAACCAGATGATGACATACATATGCTTCCAAATGGGTTCTTCTCCAT 849
 QY 284 SerLeuAlaLeuGlnGlnArgGlnHisIleGlyLeuPheArgAlaArgIle 303
 DB 850 TGTGTAGCTCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 909
 QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTyrAlaProTyrSer 323
 DB 910 TCACTGGCCATCTCTTAAAGGGTTTGTGCTTTGCTGGGCTCATATTTCT 969

QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrIleSerThrTyrIleHisThrAla 343
 DB 970 ATTGTCTTTCATTTTATTCCTCAGACAGAGGCTCTTAATCACTTTGGATG 1029
 QY 344 PheThrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyrProLeuCysHis 363
 DB 1030 TTTGGCTTCAGAGGTTCAATTCCTTGTCAATCTCTTTGTATCATGTTGTC 1089
 QY 364 ArgPheGlnIleAlaPheLeuIleValIleLeuProValArgArgGlnSerThrPro 382
 DB 1090 CGCTTTCAAAAGGCTTTCTTGAAATATTTGTATATAAAAGCACTTCACATCA 1149
 QY 383 HisAsnArgSerIleSerThr 389
 DB 1150 CACAGTCGCTCAATATCTTCT 1170

RESULT 10
 AA167750
 ID .AA167750 standard; cDNA; 1173 BP.
 XX
 AC AA167750;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Human histamine H4 receptor protein encoding cDNA.
 XX
 KW Histamine receptor; H4; antihistaminic; antiasthmatic; immunosuppressive;
 KW antiallergic; neuroprotective; antidiabetic; human;
 KW cerebroprotective; cAMP modulator; gene therapy; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..1173
 FT CDS /tag= a
 FT /product= "histamine H4 receptor"
 XX
 PN MO200185786-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 04-MAY-2001; 2001WO-US014527.
 XX
 PR 05-MAY-2000; 2000US-0202151P.
 PR 23-AUG-2000; 2000US-0227567P.
 PR 13-NOV-2000; 2000US-0247855P.
 XX
 PA (AMHP) AMERICAN HOME PROD CORP.
 XX
 PI Jones PG, Blatcher M, Wu S, Pausch MH;
 XX
 DR MPI; 2002-049442/06.
 DR P-PSDB; AAC66023.
 XX
 PT New histamine receptor, termed H4 useful for detecting H4 (ant)agonists
 PT for treating transplanted organ rejection, asthma, allergy, multiple
 PT sclerosis and rheumatoid arthritis.
 XX
 PS Claim 13; Fig 1; 66pp; English.
 XX
 CC The invention provides an isolated histamine receptor, H4, which binds
 CC ligands comprising imidazole attached to amine by an alkyl chain. The H4
 CC receptor can be expressed by standard recombinant methodology. Cells
 CC expressing H4 receptor protein at a detectable level can suppress cyclic
 CC adenosine monophosphate (cAMP) formation when contacted with the H4
 CC receptor agonist. The H4 receptor and antibodies are used for identifying
 CC H4 receptor modulators. Modulation of histamine H4 receptors is useful
 CC for treating transplanted organ rejection, asthma, allergies and
 CC autoimmune pathologies such as multiple sclerosis, type I diabetes,
 CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor
 CC protein and nucleic acids are useful targets to identify drugs that are
 CC effective in treating disorders associated with histamine-regulated

CC processes. Identification and isolation of H4 receptor provides for
 CC development of screening of molecules that interact with H4 receptors.
 CC Genetic variants of H4 can be used to diagnose an H4 associated disease
 CC as described above. The H4 receptor polynucleotide is useful to treat or
 CC prevent a disorder associated with the function of H4 in peripheral blood
 CC leukocytes. The present sequence represents a cDNA encoding the human
 CC histamine H4 receptor protein

XX
 SQ Sequence 1173 BP; 296 A; 245 C; 231 G; 401 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8,88e-119	Length:	1173
Score:	1308.50	Matches:	252
Percent Similarity:	77.52%	Conservative:	48
Best Local Similarity:	65.12%	Mismatches:	84
Query Match:	64.27%	Indels:	3
DB:	6	Gaps:	3

US-10-626-398-10 (1-389) x AA167750 (1-1173)

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OY 5 AensSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerIleu 23
DB 13 AATAGACAAATCAATTTATCACTAGACACTCGTGTACTTTAGCATTTTATGTCCTTA 72
OY 24 LeuAlaIleAlaIleuLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTTGTATATAGCTAGAAATGCTTGGTCATTTTGTAGCTTTTGTGGAGCAA 132
OY 44 AenLeuAIGHIaIArgSerAntYrPhePheLeuAenLeuAlaIleAlaAspPhePheVal 63
DB 133 AACCTTAGACATCGAAGTAGATATTTTCTTAATCTGGCAATCTGACATCTTTTGTG 192
OY 64 GIYAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpHisSerGlyAs 83
DB 193 GGTGGATCTCCATCTCTTGTACATCCCTCACAGCCTTTGGATGGATTTGGAAAG 252
OY 84 GIAlaIaCysValPheTrpLeuIleThrAspYrIleuLeuCysThrAlaSerValYrAsn 103
DB 253 GAAATCTGTATTTTGGCTCACTACTGACTATCTGTATGTAGACATCTGTATATAC 312
OY 104 IleValIleuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpYrArgAla 123
DB 313 ATGTGCTTCATCAGCATATGATGATACCTGATCTCAAGTCTCAAGCTGTATATGAAC 372
OY 124 GlnHISerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
DB 373 CAACATACCTGGGCTGTGAAGATTGTACTGTGATGTCGCGCTTGGGCTGGCTTC 432
OY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGlyCys 163
DB 433 TTAGTGAATGGGCAATGATTTCTAGTTTCAGAGTCTTGGAAAGATGAAGTAGTGA 492
OY 164 GIUPrOGIyPheLeuLysTrpYrPheAlaLeuProThrSerLeuLeuGlnPheLeu 183
DB 493 GAACCTGATTTTTCGGAATGTATACATCTTGCATCACAATCTTGTGAATTCGTG 552
OY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
DB 553 ATCCAGTATCTTACTTCCCTTATTTCAACATGAATTTATTTAGAGCTGTGGAAAGCT 612
OY 204 GIuLyLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 613 GATCATCTCTAGTAGGCGCAAGCCATCTGTGACTAGCT---GTCTCTTCAACATC 669
OY 224 HISGIyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
DB 670 TGTGACACTCATCTCAGAGTAGACTATCTTCAAGAGATCTCTTCTCATCGACAGA 729
OY 244 ThrThrAlaSerLeuGlySerAspLysSerArgLysSerSerLeuLeuProSerIle 263
DB 730 GTTCCGCAATCTTTTCATTCAGAGAGACAGAGAGAAAGTAGTAGTCAATGTTTTCCT 789
OY 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283

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DB 790 AGAACCAAGATGAATAGCAATTCATTGCTTCCAAATGGGTTCTTCCCAATCAGAT 849
OY 284 SerLeuAlaIleuGlnGlnArgLysIleGluLeuPheArgAlaArgLysLeuAlaLys 303
DB 850 TCTGTAGCTCTTCAACCAAGGACATGTGATGAGCTCAGAGCCAGAGATTAGCCAAAG 909
OY 304 SerLeuAlaIleLeuLeuAlaIlePheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
DB 910 TCACGTGGCATTTCTTGGGGGTTTGTCTGTCTTCTGGGCTCCCATATTTCTGTGTTACA 969
OY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpYrHisThrAla 343
DB 970 ATTGTCTTTCAATTTTATTTCCACCAACAGGTCCTCAATCAGTTGTAGTAAGAAATGCA 1029
OY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
DB 1030 TTTTGCTTCAGTGGTTCAATTCCTTTGTCAATCTTTTGTATTCATTTGTGTACAAAG 1089
OY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro--Pro 382
DB 1090 CGCTTCAAAAGGCTTTCTGTGAATAATTTGTATATAAAAGCAACCTCTACATCAGCA 1149
OY 389 HisAsnArgSerIleSerThr 389
DB 1150 CACAGTCGCTCAGTATCTTCT 1170
RESULT 11
ACD933262
ID ACD933262 standard; cDNA, 1173 BP.
AC933262;
ACA933262;
16-JUL-2003 (first entry)
DE Human cDNA encoding GPCR hRUP7.
XX
KW Human; ss; gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;
KW hARE-5; hRUP3; hRUP5; hRUP6; hRUP7; hGPCR27; hARE-1; hARE-2; hRUP1; hG2A;
KW hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hRUP4; signalling cascade.
OS Homo sapiens.
PN US2003017528-A1.
PD 23-JAN-2003.
XX
PF 06-JUN-2001; 2001US-00875076.
XX
PR 20-NOV-1998; 98US-0109213P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123946P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0136567P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-014148P.
PR 28-SEP-1999; 99US-0156333P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156634P.
PR 12-OCT-1999; 99US-00417044.
XX
PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LIAM/) LIAM C W.
PA (LINI/) LIN I.
XX
PI Chen R, Dang HT, Liam CW, Lin I;

```

DR WPI: 2003-428953/40.
DR p-PSDB; ABU92265.
XX
XX Novel endogenous, orphan, human G protein-coupled receptors useful for
PT identification of modulators of the receptor and as research tools for
PT understanding the role of the receptor in human body.
XX
XX Claim 25, Page 22, 54pp; English.

CC The invention relates to a human G protein-coupled receptor (GPCR) CC appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93255-ACA93274) named CC hARE-3, hARE-4, hARE-5, hRUP3, hRUP5, hRUP6, hRUP7, hGPCR27, hARE-1, hARE- CC -2, hPR1, hG2A, hCHN3, hCHN4, hCHN6, hCHN8, hCHN9, hCHN10 and hRUF4. CC Also included are a plasmid comprising a vector and one of the cDNAs CC above and a host cell comprising the plasmid. The GPCRs are useful for CC the direct identification of candidate compounds as inverse agonists, CC agonists or partial agonists. In vitro and in vivo systems incorporating CC GPCRs are useful for elucidating and understanding the roles these CC receptors play in the human condition, both normal and diseased, as well CC as understanding the role of constitutive activation as it applies to CC understanding the signalling cascade. The cDNAs are useful for making a CC probe for dot-blot analysis against tissue mRNA and/or RT-PCR CC identification of the expression of the receptor in tissue samples. The CC present sequence is a cDNA encoding a GPCR of the invention

Alignment Scores:	
Pred. No.:	8 88e-119
Score:	1208.50
Percent Similarity:	77.54%
Best Local Similarity:	65.14%
Query Match:	64.27%
DB:	8
	Gaps: 3
	Indels: 3
	Mismatches: 84
	Conservative: 48
	Matches: 252
	Length: 1173

US-10-626-398-10 (1-389) X ACA93262 (1-1173)

QY	5	AsnSerThrIleAlaLeuThr---SerIleuYsIleSerLeuThrPheLeuMetSerLeu	23
Db	13	AAATGACCAATCAATTATTCATTAAGCACTCGGTACTTAAAGCATTTTATATCCCTTA	72
QY	24	LeuAlaIleAlaIleMetLeuGluGlnValAlaValIleLeuAlaPheIleValAspArg	43
Db	73	GTAAGCTTTGCTTAATATGCTAGGAATGCTTTGGCATTTTAAAGCTTTTGTTGTGACAAA	122
QY	44	AsnLeuArgHisArgSerAsnTYrPhePheLeuAsnLeuAlaIleAlaAspPheVal	63
Db	133	AACCTTAGACATGGAAGTAGTATTTTTTTCTTAAGTGGCAGATCTGCATCTCTTG	192
QY	64	GlyAlaIleAlaIleProLeuTYrIleProSerSerLeuThrTYrTrrPheSerGlyAs	83
Db	193	GGTGTGATCTCCATTCCTTTGTATCATCCCTCACAGCTGTTCGAATGGGATTTTGGAAAG	252
QY	84	GlnAlaCysValaPheTrpLeuIleThrAspTYrLeuLeuCYrThrAlaSerValTYrAsn	103
Db	253	GAATCTGCTGATTTTGGCTCACTACGTACTCTGTTATGACGCAATCTGTTATATAC	312
QY	104	IleValleuIleSerTYrAspArgTYrGlnSerValSerAsnAlaValTrrTYrArgAla	123
Db	313	ATTGCTCTATCAAGCTATGATGCAATCCGTGACGCTCAAAATGCTGTTCTTATAGAAT	372
QY	124	GlnHisSerGlyThrTrpIysIleAlaThrGlnMetValAlaValTrrIlePheSerPhe	143
Db	373	CACATATCTGGGCTCTGAAGAATGTTCATCGATGGGCGGCTTTGGGCTGGCCCTTC	432
QY	144	MetThrAsnGlyProMetIleLeuIleSerAspSerTrrGlnAsnSerThrThrGluCys	163
Db	433	TTAGTGATAGGCGCAATGATTCAGATTTCAGAGCTTGGAGAGATGAAGTAGTAATGT	492
QY	164	GlnProGlyPheLeuIysIysTrrTYrPheAlaLeuProThrSerLeuGlnPheLeu	183
Db	493	GAACCTGGATTTTTTTCGAATGTATGATCTTGGCATCAATCATCTTGTGAATTTGTGT	552

[illegible]

PR 12-MAR-1999; 99US-0123949P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0136567P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 28-MAY-1999; 99US-0141448P.
PR 28-SEP-1999; 99US-0156533P.
PR 28-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156634P.
PR 12-OCT-1999; 99US-00417044.
XX
PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LIAM/) LIAM C W.
PA (LINI/) LIN I.
XX Chen R, Dang HT, Liam CW, Lin I;
XX
XX WPI: 2003-897571/82.
DR P-PSDB; ADG98760.
XX
XX New cDNA encoding a human G protein coupled receptor, useful for making a
PT probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR
PT identification of the expression of the receptor in tissue samples.
XX
XX Claim 25; SEQ ID NO 13; 52pp; English.

CC The present invention provides novel human G protein-coupled receptor
CC (GPCR) proteins and their encoding nucleic acids. The invention is useful
CC for making a probe for dot-blot analysis and for RT-PCR identification of
CC the expression of the receptor in tissue samples. The invention is also
CC useful for identifying candidate compounds as inverse agonists, agonists
CC or partial agonists and as research tools in determining the location of
CC the receptors within the body. The present sequence is human orphan G
CC protein-coupled receptor cDNA.

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8,886-119 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
DB: 10 Gaps: 3

US-10-626-398-10 (1-389) x ADG98759 (1-1173)

QY 5 AaSerThrIleAlaLeuThr---SerIleuYsIleSerLeuThrPheLeuMetSerIeu 23
DB 13 AATGACACATCAATTATTCACCTAGCACTGCTGATTGATTTTATATGCTCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTGCTATATATCTAGGAATGCTTGTGCTATTTAGCTTTGTGTGACAAA 132
QY 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
DB 133 AACCTTAACATCGAAGTAGTATTTTCTTAACCTTGCCATCTCGACTCTTTTGG 192
QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyAs 83
DB 193 GGTGTGATCTCATCTCTTTGTATCCCTCCACAGCTGTTGATGGATTTTGGAAAG 252
QY 84 GluAlaCysValPheTyrPheIleThrAspTyrIleLeuCysFthrAlaSerValTyrAsn 103
DB 253 GAAATCTGTGATTTTGGCTCACTAGCTATCTGTTATGTACAGCATCTGTATATAAC 312
QY 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTyrArgAla 123
DB 313 ATGTCTCATCAGCTATGATGATGATACCTGTCAAGTCTCAAAATGCTGTCTTATAGAACT 372

QY 124 GluHisSerGlyThrTrpIleAlaIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
DB 373 CAACACTACTGGGGCTTTCAGATATTTCTCTGATGAGTGGCGCTTTGGGTGCTGGCCTTC 432
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGlyCys 163
DB 433 TTAGTGAATGGCCCAATGATTTCTAGTCTTCAGAGCTTCCAGATGAGTATGTAATGT 492
QY 164 GluProGlyPheLeuValTyrTrpPheAlaLeuProThrSerLeuGlnPheLeu 183
DB 493 GAACCTGATTTTTCGGAATGGTACATCTTGGCCATCATCTTCTGSAATTCGG 552
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpIleArg 203
DB 553 ATCCACATCACTTATAGTCTGCTTATTTCAACATGATATTTATGAGCTGTGGAAGGT 612
QY 204 GluIleLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerAsp 223
DB 613 GATCATCTCAGTAGGTGCCAAAGCCATCTGACTGACTGCT---GTCCTTCCAAATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgIleGlu 243
DB 670 TGTGACACTCAATTCAGAGTACACTATCTTCAGAGAAATCTTCTGACATCAGACAGA 729
QY 244 ThrThrAlaSerLeuGlySerAspIleArgTyrSerSerLeuLeuProSerIle 263
DB 730 GTTCTGCTCATCTTTCAATTCAGAGACAGACAGAGAAAGTATGATCTATGTTTCTCTCA 789
QY 264 ArgAlaTyrIleAsnSerAsnValIleAlaSerIleMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGATATGCAATATCAATTCCTTCCAAAGGGTCTCTCCCAATCAGAT 849
QY 284 SerLeuAlaLeuGlnArgGlnHisIleGluLeuPheArgAlaArgIleLeuAlaIle 303
DB 850 TCTGAGCTCTTCACCAAGGAAACATGTGACTGCTTAGAGCCAGGATTAACAG 909
QY 304 SerLeuAlaIleLeuLeuAlaIleAlaPheAlaIleCysTrpAlaProTyrSerLeuThr 323
DB 910 TCAGTGGCCATCTTCTTGAAGGATTTTGTCTGTGCTGGGCTCCATATCTCTGTTCA 969
QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrIleSerThrTyrTrpHisThrAla 343
DB 970 ATTGCTCTTATTTATTTCTCTCAGCAACAGTCTCTTAATCATGTGTGATGAATGCA 1029
QY 344 PheTrpLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisIle 363
DB 1030 TTTTGCTTCAGTGTCAATTCCTTTGTCAATCTCTTTGTATCATTTGTGTCAAG 1089
QY 364 ArgPheGlnIleAlaPheLeuIleLeuProValArgArgGlnSerThrPro---Pro 382
DB 1090 CGCTTCAAAAGGCTTTCTTGAATAATTTGTATATAAAAGCAACCTTACATCACA 1149
QY 383 HisAsnArgSerIleSerThr 389
DB 1150 CACAGTCCGTGATATCTTCT 1170
RESULT 13
ID ABS57063 standard; cDNA, 1173 BP.
AC ABS57063;
XX
DT 28-JAN-2003 (first entry)
XX
DE Human cDNA encoding G-protein coupled receptor AXOR35.
XX Human; ss; gene; G-protein coupled receptor; AXOR35; lymphocyte;
XX macrophage; eosinophil; neutrophil; infection; transplant rejection;
XX gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;
XX Crohn's disease; irritable bowel syndrome; vomiting; inflammation;
XX atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;
XX psoriasis; urological disease; urinary retention; cardiovascular disease;

XX myocardial infarction; hypotension; hypertension; pulmonary disorder;
XX chronic obstructive pulmonary disease; cough; renal disease;
XX renal ischemia; arteriosclerosis; atherosclerosis; psychosis;
XX neurological disorder; migraine; anorexia; anxiety; schizophrenia;
XX dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;
XX graft versus host disease; osteoporosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1173
FT /tag=a
FT /product="AXOR35"
XX US2002137054-A1.
XX 26-SEP-2002.
XX 20-JUL-2001; 2001US-00910411.
XX 02-NOV-1999; 99US-00431898.
XX 03-FEB-2000; 2000US-00497790.
XX 20-OCT-2000; 2000US-00693761.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX Aubart KM, Bergsma DJ, Fitzgerald L, Graybill TL, Li X,
XX Michalovich D, Morrow DM, Zhu Y;
XX P-PSDB; ABG71960.
XX WPI; 2003-074982/07.
XX Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for
XX treating infections, gastrointestinal disorders, autoimmune disorders,
XX urological diseases, cardiovascular diseases and cancer.
XX Claim 2; Page 21-22; 24pp; English.
XX The invention relates to an isolated G-protein coupled receptor
XX polypeptide, AXOR35, (and its homologues and variants) and its encoding
XX polynucleotide (and its homologues, variants, complements and RNA
XX equivalents). Also included are an anti-AXOR35 antibody, an AXOR35
XX expression vector, producing a recombinant host cell by introducing the
XX vector into a cell such that the host cell produces AXOR35, a membrane of
XX the host cell expressing AXOR35, identifying/screening for agonists or
XX antagonists of AXOR35 and inhibiting or promoting the function of
XX lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,
XX by administering to the patient AXOR35 agonists or antagonists. The
XX agonist or antagonist identified is useful for treating a disease such as
XX asthma, or for inhibiting or promoting the function of lymphocytes,
XX macrophages, eosinophils, or neutrophils in diseased tissue such as an
XX asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays,
XX for identifying compounds that are agonists or antagonists of AXOR35, as
XX vaccines, or for treating infections (bacterial, fungal, protozoan or
XX viral infections), transplant rejection, gastrointestinal disorders (such
XX as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),
XX irritable bowel syndrome, vomiting, inflammation (such as atopic
XX dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,
XX psoriasis), urological diseases (such as urinary retention),
XX cardiovascular diseases (such as myocardial infarction), hypotension,
XX hypertension, pulmonary disorders (such as chronic obstructive pulmonary
XX disease), cough, renal diseases (such as renal ischemia),
XX arteriosclerosis, atherosclerosis, psychotic and neurological disorders
XX (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such
XX as Parkinson's disease), cancer, obesity, stroke, septic shock, graft
XX versus host disease and osteoporosis. The present sequence is the cDNA
XX encoding AXOR35
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Alignment Scores: 8.88e-119 Length: 1173
Pred. No.:

Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
DB: 10 Gaps: 3
US-10-626-398-10 (1-389) x ABS57063 (1-1173)
QY 5 AsnSerThrIleAlaLeuThr---SerIleValIleSerIleuThrPheLeuMetSerIleu 23
DB 13 AATAGCAATGCAATTAATTCATCACTGACCTGCGTGAATTCATTTTAAATGCTCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValIleValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTGCTTAATGCTAGGAATGCTTGCTATTTTACCTTTTGCGTGACAA 102
QY 44 AsnLeuArgHisArgSerAsnIlePhePheLeuAsnIleAlaIleAspPheVal 63
DB 133 AACCTTAGACATGGAAGTAGTATTTTCTTAACCTTGCCATCTGACTCTTTGTG 192
QY 64 GlyAlaIleAlaIleProLeuIleThrProSerSerIleuThrIlePheSerGlyVal 83
DB 193 GGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTCGAATGGATTTTGAAG 252
QY 84 GluAlaCysValPheThrLeuIleThrAspIleuLeuCysThrAlaSerValIleAsn 103
DB 253 GAAATCTGTATATTTGGCTCACTAGCTATCTGTATGTACAGCATCTGTATATAC 312
QY 104 IleValIleuIleSerIleAspArgIleGlnSerValSerAsnAlaValIlePheArgAla 123
DB 313 ATGTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
QY 124 GlnHisSerGlyThrIlePheIleAlaIleThrGlnMetValAlaValIlePheSerPhe 143
DB 373 CAACATACGCGGCTCTTGAAGATGTACTGTATGCTGATGCTGCTGCTGCTGCTGCTT 432
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerIleGlnAsnSerThrThruGlyCys 163
DB 433 TTAGTAATGGCAATGATTTCTAGTTTCAAGATCTTGAAGATGATGATGATGATGATGAT 492
QY 164 GluProGlyPheLeuIleuValIlePheIleAlaLeuProThrSerIleuGlnPheLeu 183
DB 493 GAACCTGATTTTTCGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 552
QY 184 IleProIleLeuLeuValAlaIlePheSerAlaHisIleIleThrSerIleuThrPheArg 203
DB 553 ATCCAGTATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 612
QY 204 GluIleLeuSerArgCysIleuSerHisProValIleuProSerAspSerSerAsp 223
DB 613 GATCATCTCAGTAGTGCCCAAGCCATCTGAGCTAGCTCT---GTCCTTCCACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrIleuProAlaArgGlyGln 243
DB 670 TGTGACACTCATTACAGAGTAGTACTTCAAGAGATCTCTTCTGATGACGACGAA 729
QY 244 ThrThrAlaSerIleuIleSerAspIleSerArgArgIleSerSerIleuProSerIle 263
DB 730 GTTCTGCTGATCTTCTTATTCAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 789
QY 264 ArgAlaIleIleAsnSerAsnValIleAlaSerIleMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 849
QY 284 SerLeuAlaLeuGlnIleArgGlnIleGlnIleGlnIlePheArgAlaArgIleuAlaGly 303
DB 850 TGTGTAGCTCTTACACCAAGGAAACATGTTGAAGCTCTTAGACCCAGGAAATTAGCCAG 909
QY 304 SerLeuAlaIleLeuLeuAlaIlePheAlaIleCysThrAlaProIleSerIleuThr 323
DB 910 TCACTGCGCATTTCTTGAAGGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969
QY 324 ValIleIleSerPhePheProGluArgAsnIleuThrIleSerThrIlePheIleAla 343

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Db      970  ATGTGCTTTCAATTTATCTCAGCAACAGGCTCCAAATCAGTTGGTATGATGCA 1029
      344  PheTPlEuGIntTrPheNsSerPheValaNsProPheLeuTyProLeuGyHisIys 363
      1030  TTTGGCTTCAGTGGTTCATTCCTTTGCAATCCCTTTTATCCATGTCACAAAG 1089
Qy      364  ArgPheGlnIyAlaPheLeuIyIleLeuProValaArgArgGlnSerThrPro--Pro 382
Db      1090  CGCTTCAAAAGGCTTTCTTGAAAATATTTGTATATAAAAGCAACCTTACCACACACA 1149
Qy      383  HisaenArgSerIleSerThr 389
      1150  CACAGCTCGTCAGTATCTTCT 1170
RESULT 14
ADJ26922
ID      ADJ26922 standard, cDNA, 1173 BP.
XX
AC      ADJ26922;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Human endogenous orphan G-protein coupled receptor RUP7 cDNA.
XX
KM      Human; G protein-coupled receptor; GPCR; dot-blot analysis;
XX      pharmaceutical agent; gene; ss.
XX
OS      Homo sapiens.
XX
Key      Location/Qualifiers
FT      CDS             1..1173
FT      CDS             /*tag= a
FT      FT              /product= "Human endogenous orphan GPCR protein"
XX
PN      US2003175891-A1.
XX
PD      18-SEP-2003.
XX
PF      21-MAR-2003; 2003US-00393807.
XX
PR      20-NOV-1998; 98US-0109213P.
PR      16-FEB-1999; 99US-0120416P.
PR      26-FEB-1999; 99US-0121852P.
PR      12-MAR-1999; 99US-0123946P.
PR      12-MAR-1999; 99US-0123949P.
PR      28-MAY-1999; 99US-0136436P.
PR      28-MAY-1999; 99US-0136437P.
PR      28-MAY-1999; 99US-0136439P.
PR      28-MAY-1999; 99US-0136567P.
PR      28-MAY-1999; 99US-0137127P.
PR      28-MAY-1999; 99US-0137131P.
PR      29-JUN-1999; 99US-0141448P.
PR      28-SEP-1999; 99US-0156333P.
PR      29-SEP-1999; 99US-0156555P.
PR      29-SEP-1999; 99US-0156634P.
PR      29-SEP-1999; 99US-0156653P.
PR      01-OCT-1999; 99US-0157280P.
PR      01-OCT-1999; 99US-0157282P.
PR      01-OCT-1999; 99US-0157293P.
PR      01-OCT-1999; 99US-0157294P.
PR      12-OCT-1999; 99US-00417044.
PR      17-OCT-2002; 2002US-00272983.
XX
PA      (CHEN/) CHEN R.
PA      (DANG/) DANG H T.
PA      (LIAM/) LIAM C W.
PA      (LINI/) LIN I.
PI      Chen R, Dang HT, Liaw CW, Lin I,
XX      WPI; 2003-898539/82.
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DR      P-PSDB; ADJ26923.
XX
XX      New human G protein-coupled receptor and its coding cDNA, useful for
PT      disease or disorder identification and/or selection, for screening of
PT      candidate compounds useful as pharmaceutical agents, and in research
PT      applications.
XX
PS      Claim 25; SEQ ID NO 13; 53pp; English.
XX
CC      The present invention relates to human endogenous orphan G protein-
CC      coupled receptor (GPCR) proteins and polynucleotides encoding such
CC      proteins. The cDNA sequence of the human G protein-coupled receptor
CC      (GPCR) is useful in making a probe for dot-blot analysis against tissue-
CC      mRNA and/or for RT-PCR identification of the expression of the receptor
CC      in tissue samples. GPCR sequences of the invention may be used in
CC      disease/disorder identification and/or selection, in screening of
CC      candidate compounds for use as pharmaceutical agents and in research
CC      settings. The present sequence is human endogenous orphan GPCR cDNA.
XX
SQ      Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 8,88e-119 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
DB: 11 Gaps: 3
US-10-626-398-10 (1-389) x ADJ26922 (1-1173)
Qy      5 AenSerThrIleAlaLeuThr---SerIleIySleSerLeuThrPheLeuMetSerLeu 23
Db      13 AATAGCACATCAATTAATTACACTAGCACTGCTTACTTATGCAATTTTATGTCCTTA 72
Qy      24 LeuAlaIleAlaIleMetLeuGlyAsnValValAlIleLeuAlaPheIleValaSpArg 43
Db      73 GTAGCTTTTGCTATATATGCTAGGAATGCTTGTGTCATTTTGCTTGTGTGGAGCAAA 132
Qy      44 AenLeuARGHsARGSerAsnTyRPhPheLeuAenLeuAlaIleAlaAspPheVal 63
Db      133 AACCTTAGACATCGAAGTAGTATTTTCTTAATCTGGCCATCTGACCTCTTTG 192
Qy      64 GlyAlaIleAlaIleProLeuTyRleProSerSerLeuThrTyRTrpThrSergIyS 83
Db      193 GGTGTGATCTGCATTCCTTTGTACATCCCTCACAGCGCTTGGAATGGATTTGGAAAG 252
Qy      84 GlnAlaCyValPheTrpLeuIleThrAspTyRLeuLeuCyThrAlaSerValTyRAsn 103
Db      253 GAATCTGTGATTTTGGCTCACTACTGATCTGATATGTTATGACGATCTGATATATAC 312
Qy      104 IleValIleIleSerTyRAspArgTyRArgIleValSerAsnAlaValTrpTyRAla 123
Db      313 ATTTGCTTCATCAGCTATGATGATGATCCTGTCAGTCTCAATAGCTGTGCTTAAGAACT 372
Qy      124 GlnHisSergIyThrTrpIySleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
Db      373 CAACATACCTGGGGCTTGGAAGTTGTTACTCTGAGTGGTGGCGCTTGGGTGGCGCTTC 432
Qy      144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrArgIuCyS 163
Db      493 TTAGGAATGGGCCAATATCTACTTTCAGAGCTCTGGAAGATGAAGTAGGTGATGT 492
Qy      164 GluProGlyPheLeuIyLeuTyRTrpTyRPhAlaLeuProThSerLeuLeuGluPheLeu 183
Db      493 GAACCTGGATTTTTCGGAATGGTACATCTTGCCATCACAATCTTGGAAATTCGG 552
Qy      184 IleProIleLeuLeuValAlaTyRPhSerAlaHisIleTyRTrpSerLeuTrpIySArg 203
Db      553 ATCCAGTCATCTTAGTGCTTATTTCAACATGAATATTATTTAGAGCCTGGAAAGCT 612
Qy      204 GluIySleuSerArgCyLeuSerHisProValIleuProSerAspSerSerSerAsp 223
DB: 11 Gaps: 3
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Db      613 GATCATCTCAGTAGTGCCAAAGCCATCTCGACTGCTCTCTTCCCAATC 669
Qy      224 HlaGLVHiserCybarglnaProAspSerArgAlaThrleuProAlaArglyGlu 243
Db      670 TGTGGACCTCATTCAGAGGTAGACTATCTTCAAGGATCTCTTGTGATGACAGAA 729
Qy      244 ThrThraLaserleuGlySerApLySerArgArglySerSerleuProSerile 263
Db      730 GTTCCTGCATCTTTCATTCAGAGAGACAGAGGAAAGTGTCTCATGTTTCTCTCA 789
Qy      264 ArgAlaLtyrLysAsnSerAsnVal11aLaserLysMetGlyPheLeuSerHisSerAsp 283
Db      790 AGAACCAAGATGATGACATACAAATGCTTCCAAATGGGCTCTTCCCATCATGAT 849
Qy      284 SerLeuAlaLeuGlnGlnArgGluHisGleGluLeuPheArgAlaArglyLysLeuAlaLys 303
Db      850 TCTGTACCTTTCACCAAGGAAATGTAAGTCTTGAAGCCAGAGACATTAAGCCAG 909
Qy      304 SerLeuAlaLeuLeuAlaAlaPheAlaAlaLeuCystrPalaProTyrSerLeuThrThr 323
Db      910 TCACGTGGCATTCTCTTAGGGGTTTTCGCTTGTGCTGGGCTCCATATCTCTGTTACA 969
Qy      324 Val11eTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrrPlyHisThrAla 343
Db      970 ATTGTCTTTCATTTATTCCTCAGCAACAGTCTTAATCACTTGTGTATGATTCGA 1029
Qy      344 PheTyrLeuGlnTrrPheAsnSerPheValAsnProPheLeuTyrProLeuCystrLys 363
Db      1030 TTTTGCTTCAGGGTTCATCTCTTGTCAATCTCTTGTATTCATTTGTGTACAG 1089
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Db      1090 CGCTTCAAAAGCTTCTTGAATAATTTGTATATAAAAGCAACCTCATCATCACAA 1149
Qy      383 HisAsnArgSerLysSerThr 389
Db      1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 15
ID      ADG86374 standard; cDNA; 1173 BP.
XX      ADG86374;
AC      11-MAR-2004 (first entry)
DT      Human endogenous orphan GPCR hRUP7 cDNA.
XX      Human; ss; gene; endogenous orphan GPCR; G protein-coupled receptor;
KW      transmembrane domain 6.
XX      Homo sapiens.
PN      US2003229216-A1.
PD      11-DEC-2003.
XX      16-APR-2003; 2003US-00417820.
XX      13-OCT-1998; 98US-00170496.
PR      12-NOV-1998; 98US-0108029P.
PR      20-NOV-1998; 98US-0109213P.
PR      27-NOV-1998; 98US-0110060P.
PR      16-FEB-1999; 99US-0120416P.
PR      26-FEB-1999; 99US-0121852P.
PR      12-MAR-1999; 99US-0123944P.
PR      12-MAR-1999; 99US-0123945P.
PR      12-MAR-1999; 99US-0123948P.
PR      12-MAR-1999; 99US-0123949P.
PR      12-MAR-1999; 99US-0123951P.
PR      28-MAY-1999; 99US-0136436P.
PR      28-MAY-1999; 99US-0136437P.

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PR      28-MAY-1999; 99US-0136439P.
PR      28-MAY-1999; 99US-0136567P.
PR      28-MAY-1999; 99US-0137127P.
PR      28-MAY-1999; 99US-0137131P.
PR      28-MAY-1999; 99US-0141448P.
PR      27-JUN-1999; 99US-0151114P.
PR      27-AUG-1999; 99US-0152524P.
PR      03-SEP-1999; 99US-0156555P.
PR      29-SEP-1999; 99US-0156633P.
PR      29-SEP-1999; 99US-0156634P.
PR      29-SEP-1999; 99US-0156635P.
PR      01-OCT-1999; 99US-0157280P.
PR      01-OCT-1999; 99US-0157281P.
PR      01-OCT-1999; 99US-0157282P.
PR      01-OCT-1999; 99US-0157293P.
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PR      12-OCT-1999; 99US-00416760.
XX      (CHEN/) CHEN R.
PA      (LIAM/) LIAM C W.
PA      (LOWITZ/) LOWITZ K.
PA      (CHAL/) CHALMERS D T.
PA      (BEHA/) BEHAN D P.
XX      Chen R, Liam CW, Lowitz K, Chalmers DT, Behan DP;
PI      WPI: 2004-052038/05.
XX      P-PSDB; ADG86375.
DR      New cDNA encoding a non-endogenous, constitutively activated version of a
XX      human G protein-coupled receptor, useful for identifying receptor,
PT      inverse or partial agonists having potential applicability as therapeutic
PT      agents.
XX      Example 1; SEQ ID NO 13; 110pp; English.
XX      The invention relates to a cDNA encoding a non-endogenous, constitutively
XX      activated version of a human G protein-coupled receptor comprising hARE-
XX      3 (F313K), hARE-4 (V233K), hARE-5 (A240K), hGPCR14 (I257K), hGPCR27 (G283K),
XX      hARE-1 (E232K), hARE-2 (G285K), hPR1 (L239K), hG2A (K232A), hRUP3 (L224K),
XX      hRUP5 (A236K), hRUP6 (N267K), hRUP7 (A302K), hCHN4 (V236K), hMC4 (V244K),
XX      hCHN5 (S284K), hCHN6 (L352K), hCHN8 (N235K) or h9 (F236K). Also included are
XX      a non-endogenous version of a human G protein-coupled receptor encoded by
XX      the cDNA, a plasmid comprising the vector and the cDNA and a host cell
XX      comprising the plasmid. The cDNA encodes a non-endogenous, constitutively
XX      activated version of a human G protein-coupled A11 receptor comprising
XX      the angiotensin II type 1 receptor hAT1 (F239K), hAT1 (N111A),
XX      hAT1 (ATXK251C3), a domain swap mutant) or hAT1 (A243K). The mutation is of
XX      an amino acid 16 residues from the proline in transmembrane domain 6 and
XX      is usually to a lysine. The cDNA is useful for identifying candidate
XX      compounds as receptor agonists, inverse agonists or partial agonists
XX      having potential applicability as therapeutic agents. The present
XX      sequence is a cDNA (or fragment) for a wild-type human GPCR.
XX      SQ      Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      8,88e-119      Length:      1173
Score:          1308.50      Matches:      252
Percent Similarity: 77.52%      Conservative: 48
Best Local Similarity: 65.12%      Mismatches: 84
Query Match:      64.27%      Indels:      3
DB:              12      Gaps:      3

US-10-626-398-10 (1-389) x ADG86374 (1-1173)
Qy      5 AsnSerThr11eAlaLeuThr---Ser11eLysSerLeuThrPheLeuMetSerLeu 23
Db      13 AATAGCAATCATTCATTCACACAGCACTCGTCTACTTACGATTTTATAGTCTTA 72
Qy      24 LeuAla11eAlaLeuMetLeuGlnArgAsnVal11aLaserLysMetGlyPheLeuSerHis 43
Db      73 GTAGCTTTGCTTATATGCTAGGAATGCTTGTGTCATTTTACCTTTTGTGTGACAA 132

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QY 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
DB 133 AACCTTAGACATCGAAGTAGTATTTTCTTAACCTTGCCATCTGCACCTCTTGCG 192
QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTyrThrSerGlyLys 83
DB 193 GGTGGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTCGAATGGGATTTGGAAAG 252
QY 84 GlnAlaCysValPheThrLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
DB 253 GAAATCTGTATTTTGGCTACTGACTGATCTGATCTGTATGTACAGCATCTGTATATAC 312
QY 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrPyrArgAla 123
DB 313 ATTGCCTCATCAGCATATGATCGATACCTGTCAGTCTCAATGCTGTCTTATAGAACT 372
QY 124 GlnHisSerGlyThrTyrLysIleAlaThrGlnMetValAlaValTyrIlePheSerPhe 143
DB 373 CAACATACTGGGGCTGTGAAGATTGTACTGTATGATGTCGCCGTTGGGCTCGCCCTTC 432
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTyrGlnAsnSerThrThrGlyCys 163
DB 433 TTAGGAATGGGCCAATGATTTAGTTTCAGAGTCTTGSAGAGATGAAGCTATGAAATGT 492
QY 164 GluProGlyPheLeuLysIleTyrTyrPheAlaLeuProThrSerLeuGluPheLeu 183
DB 493 GAACTGGATTTTTCGGAATGTATCATCTTGCCATCACAATCTCTTGGAATTCGTG 552
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTyrSerLeuTyrLysArg 203
DB 553 ATCCAGATCATCTTGTGCTTATTTTCAACATGAATATTATTATGGAGCTGTGGAAGCGT 612
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 613 GATCATCTCAGTAGGTGCGAAAGCATCTCGACATGACTGCT--GTCCTTTCACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
DB 670 TGTGACACTCATTCAGAGTAGATCTTCAAGAGATCTCTTCTGCAATCGACAGAA 729
QY 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
DB 730 GTTCTCGCATCTTTCATTCAGAGACAGAGAGAAAGATGATCTCATGTTCCTCA 789
QY 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGAAATAGCAATTCATTCCTCCAAATGGGTTCTTCTCCAAATCAGAT 849
QY 284 SerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
DB 850 TCTGTAGCTCTCACCAAGGGAACATGTTGAACGCTTAGAGCCAGAGATTAGCCAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTyrAlaProTyrSerLeuThrThr 323
DB 910 TCACCTGGCCATCTCTTAGGGGTTTGTGCTGTGCTGGCTCCATATCTCTGTTCACA 969
QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTyrTyrHisThrAla 343
DB 970 ATTGTCTTTCATTTTATTCCTCAGCAACAGGCTCTAAATCAGTTTGGTATAGAAATGCA 1029
QY 344 PheTyrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
DB 1030 TTTTGGCTTCAGTGGTCAATTCCTTGTCAATCCTTTTGTATCATTGTGTCAACAAG 1089
QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro--Pro 382
DB 1090 CGCTTTCAAAAGGCTTTCTTGAAAATATTGTATAAAAAGCAACCTCTACATCACAA 1149
QY 383 HisAsnArgSerIleSerThr 389
DB 1150 CACAGTCGGTCAGATCTTCT 1170
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Search completed: August 5, 2005, 20:42:36
Job time : 596 secs

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SUMMARIES

OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
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Title: US-10-626-398-10
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Delop 6.0 , Delext 7.0

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Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS-human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=ext -THR MAX=100
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Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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- 19: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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- 24: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
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3	2025	99.5	1170	21	US-10-626-398-7
4	1308.5	64.3	1173	9	US-09-812-216-1
5	1308.5	64.3	1173	9	US-09-910-411-1
6	1308.5	64.3	1173	10	US-09-875-076-13
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11	1308.5	64.3	1173	16	US-10-393-807-13
12	1308.5	64.3	1173	17	US-10-417-820A-13
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17	1308.5	64.3	1173	20	US-10-626-445-1
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22	1308.5	64.3	1300	10	US-09-852-165-1
23	1308.5	64.3	1300	19	US-10-696-673-1
24	1308.5	64.3	3689	15	US-10-225-567A-628
25	1308.5	64.3	3689	21	US-10-684-206-19
26	1306.5	64.2	1173	15	US-10-290-078-26
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44	689.5	33.9	2050	21	US-10-759-463-21
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ALIGNMENTS

RESULT 1
US-10-626-445-7
; Sequence 7, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27

Pred. No. is the number of results predicted by chance to have a

SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Cavia porcellus
US-10-626-445-7

Alignment Scores:

Pred. No.:	3.48e-219	Length:	1170
Score:	2025.00	Matches:	388
Percent Similarity:	99.74%	Conservative:	0
Best Local Similarity:	99.74%	Mismatches:	1
Query Match:	99.46%	Indels:	0
DB:	20	Gaps:	0

US-10-626-398-10 (1-389) x US-10-626-445-7 (1-1170)

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Db 1 ATGTTGGCAAAATACAGTACATCGCTTACATCAATTAATTTCTTTGACATTTTAA 60
OY 21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIle 40
Db 61 ATGCTTTTACTGCTAATGCTAATGTAAGCAATGTCGTGCTATTACCTTTTATT 120
OY 41 ValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAsp 60
Db 121 GTGGACAGAAATCTTAGACATCGAAGTAACTTTTCTTTTCTTACCTGGCCATTGGAGAC 180
OY 61 PhePheValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80
Db 181 TTCTTTGGGGTGCAATTCGAATTCCTCTGTACATACCTTCCTCGTGCATTACTGAGACT 240
OY 81 SerGlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuGlyThrAlaSer 100
Db 241 TTGGAAACAGCTTGTTGTAATTTGGCTTACTGACTTATCTTTTATGTACAGCATCT 300
OY 101 ValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrp 120
Db 301 GTGTAAATATATTGTCCTCATCAGCTACGATCGCTACGATCGTCAATATGCCGTGTG 360
OY 121 TTTAAGAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIle 140
Db 361 TATAGAGCTCAGACACTCTGACCTGGAAATTTGCTACACATGTGTGCTGTGTGGA 420
OY 141 PheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThr 160
Db 421 TTCTCTTTCATGACAAATGGCCGATGATTCGATTTTCAGACTCTTTGGCAGAAATGACT 480
OY 161 ThrGluCysGluProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuLeu 180
Db 481 ACAGAAATGGAACCTGGATTTTAAAAAGTGTACTTGTCTCTCCCTACATCATTTATG 540
OY 181 GluPheLeuIleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeu 200
Db 541 GAATTCCTGATCCCATCTTGTAGTTGCTTATTTTCAGGCCCATATTTACGAGCCCTG 600
OY 201 TrpLysArgGluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSer 220
Db 601 TGGAAAGCCAGAAACTGACAGGTGCTCTCAGCCACTGTACTCCCTCTGACTCTTCTC 660
OY 221 SerSerAspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAla 240
Db 661 AGCAGTACACAGGACACTCCTGCAGACAGGACCCCGATTCAAGGGCGACTCTGCAGACA 720
OY 241 ArgLysGluThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeu 260
Db 721 CGGAAGAAACAACCTGCTCTCTTGTGTTGACAACTCAACGAGAAAGGCAAGTCTCTTG 780
OY 261 ProSerIleArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSer 280
Db 781 TTTTTCATTAAGACCTTACAAAGAACGCAATGTGATGCTTCCAAATATGGGCTTCTCTC 840
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OY 301 LeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSer 320
Db 901 TTAGCCAAATCAGCTGGCCATCTTTCAGACGCTTTTGGCATTGTGGGCTCAATATCA 960
OY 321 LeuThrTrpValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyr 340
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OY 341 HisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeu 360
Db 1021 CATACTGCCCTTTGGCTCCAGGTGTTCAATTCCTTGTGTTAATCCCTTTTGTATCCATTG 1080
OY 361 CysHisLysArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgLysSerThr 380
Db 1081 TGTCACAAAACGTTTTCAGAAAGCTTTCCTGAAAATATCTTCTGTGAGAAAGCAATCCAG 1140
OY 381 ProProHisAsnArgSerIleSerThr 389
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RESULT 2
US-10-626-126-7
; Sequence 7, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Cavia porcellus
US-10-626-126-7

Alignment Scores:
Pred. No.: 3.48e-219 Length: 1170
Score: 2025.00 Matches: 388
Percent Similarity: 99.74% Conservative: 0
Best Local Similarity: 99.74% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: 21 Gaps: 0

US-10-626-398-10 (1-389) x US-10-626-126-7 (1-1170)
OY 1 MetLeuAlaAsnAsnSerThrIleAlaLeuThrSerIleValIleSerLeuThrPheLeu 20
Db 1 ATGTTGGCAAAATACAGTACATCGCTTACATCAATTAATTTCTTTGACATTTTAA 60
OY 21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIle 40
Db 61 ATGCTTTTACTGCTAATGCTAATGTAAGCAATGTCGTGCTATTACCTTTTATT 120
OY 41 ValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAsp 60
Db 121 GTGGACAGAAATCTTAGACATCGAAGTAACTTTTCTTTTCTTACCTGGCCATTGGAGAC 180
OY 61 PhePheValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80
Db 181 TTCTTTGGGGTGCAATTCGAATTCCTCTGTACATACCTTCCTCGTGCATTACTGAGACT 240
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QY      101 ValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAlaValTyr 120
Db      301 GGTGTAATAATATTTCTTCATCAGCTACGATGAGTCCAGCACTCAATGCGGTGG 360
QY      121 TyrArgAlaGlnHisSerGlyThrTrpValIleAlaThrGlnMetValAlaValTyrPile 140
Db      361 TATAGAGCTCAGACCTGTGGCACTGGAAATTGCTACTAGATGGTGGCTTTGGATA 420
QY      141 PheSerPheMetThrAnglyPrometIleLeuIleSerAspSerTyrGlnAsnSerThr 160
Db      421 TTCTCCTTCAAGCAATGGCCGATGATCTGATTTCAGACTCTTGCGCAATAGCACT 480
QY      161 ThrGluCysGluProGlyPheLeuIleValTyrTyrPheAlaLeuProThrSerLeuLeu 180
Db      481 ACAGAAATGGAACCTGGATTTTAAAGTGGTACTTTCCTCTCCATCATATTATG 540
QY      181 GluPheLeuIleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeu 200
Db      541 GAATTCCTGATCCCATCTTTGTTGTTGCTTATTTCAGCCCAATTATTACTGGAGCTG 600
QY      201 TrpTyrArgGluValysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSer 220
Db      601 TGGAAAGAGAGAACTGAGCAGAGTGGCTCAGCACTGCTACTCCCTCTGACTCTTCC 660
QY      221 SerSerAspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAla 240
Db      661 AGAGAGGACCAAGCACTCTCCAGACAGAGCCCCGATTCAGAGGGGAGACTCGCCAGCA 720
QY      241 ArgGlyGluThrThrAlaSerLeuGlySerAspIleSerArgArgIleSerSerLeuLeu 260
Db      721 CGAGAAAGAAACACTGCTCTCTTGGTTCCAGACAGTCAAGAGAAAGACAGACTCTTGG 780
QY      261 ProSerIleArgAlaTyrIleAsnSerAsnValIleAlaSerIleMetGlyPheLeuSer 280
Db      781 TTTTCATATAAGACCTTCAAGAAACAGCAATGTGATGCTTCGAAATGGGCTTCTCTCC 840
QY      281 HisSerAspSerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgIle 300
Db      841 CACTCGATTTCCCTGGCTCTTTCAGCAAGGAAACATTCGAACTTTTCAGAGCCAGGAAA 900
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QY      321 LeuThrThrValIleTyrSerPhePheProGluArgAsnLeuThrIleSerThrTyr 340
Db      961 CTGACTACAGATTTCATCTCATTTTTCCTGAAAGAACTTGACTGAATCAACTGGTAC 1020
QY      341 HisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeu 360
Db      1021 CATACAGCCCTTTGGCTCCAGTGGTTCATTTCTTTGTTAATCCCTTTTGTATCATTTG 1080
QY      361 CysHisIleValArgPheGlnIleValAlaPheLeuValIleLeuProValArgArgIleSerThr 380
Db      1081 TGTCAAAAGCGTTTTCAGAAAGGCTTTTCGAAATACTTCTCTGTGAAAGGCAATCCACG 1140
QY      381 ProProHisAsnArgSerIleSerThr 389
Db      1141 CCACCAACACACCGCTCAATATCTCACT 1167

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; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Cavia porcellus
; US-10-626-398-7

Alignment Scores:
Pred. No.:      3,48e-219      Length:      1170
Score:          2025.00      Matches:      388
Percent Similarity: 99.74%      Conservative: 0
Best Local Similarity: 99.74%      Mismatches: 1
Query Match:    99.46%      Indels:      0
DB:             21          Gaps:          0

US-10-626-398-10 (1-389) x US-10-626-398-7 (1-1170)

QY      1 MetLeuAlaAsnAsnSerThrIleAlaLeuThrSerIleValIleSerLeuThrPheLeu 20
Db      1 ATGTTGGCAATATACAGTACATCGCCTTACATCAATTAATTTCTTGGACATTTTGA 60
QY      21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIle 40
Db      61 ATGCTTTACTACCTTATGCTATTAATGTTAGCAATGTCGTGCTCAATTTAGCTTTAT 120
QY      41 ValAspArgAsnLeuArgHisArgSerAsnTyrPhePheAsnAsnLeuAlaIleAlaAsp 60
Db      121 GTGAGCAAGAAATTTAGACATTCGACGAAATTAATTTCTTTTCACTTGGCAATGGAC 180
QY      61 PhePheValGlyValIleAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80
Db      181 TTTCTTGTGGGTGCATTTGCAATTCCTCTGTACATACCTTCCCTGGTCACTTGTGACT 240
QY      81 SerGlyValGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSer 100
Db      241 TCTGGAAGACGACTGTGTATTTGGCTCATTACTGACTATCTTTATGTACAGCATCT 300
QY      101 ValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAlaValTyr 120
Db      301 GGTGTAATAATATTTCTTCATCAGCTACGATGAGTCCAGCACTCAATGCGGTGG 360
QY      121 TyrArgAlaGlnHisSerGlyThrTrpValIleAlaThrGlnMetValAlaValTyrPile 140
Db      361 TATAGAGCTCAGACCTGTGGCACTGGAAATTGCTACTAGATGGTGGCTTTGGATA 420
QY      141 PheSerPheMetThrAnglyPrometIleLeuIleSerAspSerTyrGlnAsnSerThr 160
Db      421 TTCTCCTTCAAGCAATGGCCGATGATCTGATTTCAGACTCTTGCGCAATAGCACT 480
QY      161 ThrGluCysGluProGlyPheLeuIleValTyrTyrPheAlaLeuProThrSerLeuLeu 180
Db      481 ACAGAAATGGAACCTGGATTTTAAAGTGGTACTTTCCTCTCCATCATATTATG 540
QY      181 GluPheLeuIleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeu 200
Db      541 GAATTCCTGATCCCATCTTTGTTGTTGCTTATTTCAGCCCAATTATTACTGGAGCTG 600
QY      201 TrpTyrArgGluValysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSer 220
Db      601 TGGAAAGAGAGAACTGAGCAGAGTGGCTCAGCACTGCTACTCCCTCTGACTCTTCC 660
QY      221 SerSerAspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAla 240
Db      661 AGAGAGGACCAAGCACTCTCCAGACAGAGCCCCGATTCAGAGGGGAGACTCTGCGAGCA 720
QY      241 ArgGlyGluThrThrAlaSerLeuGlySerAspIleSerArgArgIleSerSerLeuLeu 260

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RESULT 3
US-10-626-398-7
; Sequence 7, Application US/10626398
; Publication No. US2005007484A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034

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Db	721	CGAAGAACAACACTGCTCTTGGTTCA	GACAAAGTCACGGAAGAAAGCAGTCTTGG	780
Qy	261	ProSerIleAlaGlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSer		280
Db	781	TTTTTCATAGAGCCTTACAGAACAGCAATGTGATCGCTCCAAATGGGCTTCCTCC		840
Qy	281	HisSerAspSerLeuAlaLeuGlnInArgIleHisIleGluLeuPheArgAlaArgLys		300
Db	841	CACCTAGATTCCTGGCTCTTCACGAAAGGAAACATTCAGAACTTTCACAGCCAGGAAA		900
Qy	301	LeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSer		320
Db	901	TTAGCGAAGTCACTGGCCATCTCTTACAGACTTTTGGCAATTTGCTGGGCTCCATATTCA		960
Qy	321	LeuThrThrValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTyrPyr		340
Db	961	CTGACTACAGTATCTACTCATTTTTCCTGAAAGAACTGACTAAATCAACTGGTAC		1020
Qy	341	HisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeu		360
Db	1021	CATACGCTTTTGGCTCCAGTGGTCAATTCTTTGTATATCCTTTGTATATCCATG		1080
Qy	361	CysHisLysAspPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThr		380
Db	1081	TGTCAACAACGTTTTCAGAAAGGCTTTCTGAAATAATCTTCTGTGAGAAAGCAATCCACG		1140
Qy	381	ProProHisAsnArgSerIleSerThr		389
Db	1141	CCACCACACAAACCGTCAATATCCACT		1167

RESULT 4
US-09-812-216-1

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Sequence 1, Application US/09812216
Patent No. US20020098539A1
GENERAL INFORMATION:
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Laz, Thomas M.
APPLICANT: Monema, Frederick J. Jr.
APPLICANT: Morse, Kelley L.
APPLICANT: Umland, Shelby P.
APPLICANT: Wang, Suke
TITLE OF INVENTION: Histamine receptor
FILE REFERENCE: CN01059
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/414,010
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-09-812-216-1

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Alignment Scores:	
Pred. No.:	8.77e-138
Score:	1308.50
Percent Similarity:	77.52%
Best Local Similarity:	65.128
Query Match:	64.27%
DB:	9
	9
	Gaps:
	3
	3
	1173
Length:	1173
Matches:	252
Conservative:	48
Mismatches:	84
Indels:	
Gaps:	3

US-10-626-398-10 (1-389) x US-09-812-216-1 (1-1173)

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OY   ASMSSErhllealeutrr---SeLlalyelaserleuthrheluewetserlu 23
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
D6   AATGCGACATTCATTATCATAGAGACTGGGTGTACTTTACCACTTTTAACTCCTTA 72
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY   LeunlaalleallewettlenGLlyAsnValVallleunlabhellevaasparg 43
      ::||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ::|||
```

D	73	GTAGCTTTTGGTAAATGCTAGAAATGCTTTGGCATTTAGCTTTTGGTGGCAAA	132
Q	44	AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaLeuAspPheVal	63
D	133	AACTTGAACATGCAGATGATATATTTTCTTAATCTTGGCACTCTGACTCTTTGGT	192
Q	64	GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpHisSerGlyAs	83
D	193	GGTGGATCTTCATCTCTTTTACATCCCTCACAGCTTTCGAATGGGATTTTGGAAAG	252
Q	84	GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn	103
D	253	GAATTCGTGATATTTTGGCTCAGTACGACTATCTGTTATGACAGCATCTGTATATAC	312
Q	104	IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTyrArgAla	123
D	313	ATTGTCCTCATCAGCTATGATCGATACCTGTCAGTCTCAATAGCTGTCTTATGAACT	372
Q	124	GlnHisSerGlyThrTrpPheIleAlaThrGlnMetValAlaValTrpIlePheSerPhe	143
D	373	CAACATCTGGGGTCTGAAGATTGTACTGTGATGGTGGCGCTTTGGGTCTGGCCCTTC	432
Q	144	MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGlyCys	163
D	433	TTAGTGAATGGGCCAAATGATTTCTAGTTCTCAGAGCTTGGAAAGATGAAGTGAATGT	492
Q	164	GlnProGlyPheLeuLysLysTyrTyrPheAlaLeuProHisSerLeuLeuGlnPheLeu	183
D	493	GAACCTGGATTTTTCGAAATGGTATACCTCTTCCATCATCATCATCTTGGAAATTCGTG	552
Q	184	IleProIleLeuLeuValAlaTyrPheSerSerAlaHisIleTyrTrpSerLeuTrpLysArg	203
D	553	ATCCAGCATCTTAGTCGCTTATTTCAACATGAATATTTATGGAGCTGTGGAAAGGT	612
Q	204	GlnLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp	223
D	613	GATATCTCAGTAGAGTGCACAAAGCATCTTGAGTACTGCT---GTCCTTCCAACTC	669
Q	224	HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu	243
D	670	TGTGACACCTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTTCGATCGACAGA	729
Q	244	ThrThrAlaSerLeuGlySerAspLysSerArgAlaArgLysSerSerLeuLeuProSerIle	263
D	730	GTTCCTCGATCTCTTTCATTCAGAGACAGAGGAGAAAGATAGTCTCATGTTTCCCA	789
Q	264	ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp	283
D	790	AGAACCAAGATGAATAGCATACATCAATGCTTCCAAATGGGTCTCTCCCAATGCAT	849
Q	284	SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys	303
D	850	TCTGTACTCTTTCACCAAGAGGAATCATGTTGAACTGCTTAGAGCAGAGATTTAGCCAA	909
Q	304	SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr	323
D	910	TCAGTGGCAATCTCTTAAGGGGTTTTGGCTGTGGCTGCATATTTCTCTGTCCACA	969
Q	324	ValIleLysSerPhePheProGlnArgAsnLeuThrLysSerThrTrpTyrHisIleThrAla	343
D	970	ATTGTCTCTTCAATTTATCTCTCAGCAACAGCTCTAAATCATAGTTGGTATAGAAATGCA	1029
Q	344	PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys	363
D	1030	TTTTGGCTTCACTGCTCATCTCTTTGTCAATCTCTTTTGATTCATCTGTGTACAAAG	1089
Q	364	ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro--Pro	382
D	1090	CGCTTCAAAAGGCTTCTGAAATATTTTGATATAAAAGCAACCTTCATCATCAAA	1149
Q	383	HisAsnArgSerIleSerThr 389	
D	1150	CACAGTGGGTCAGATCTTCT 1170	

RESULT 5
US-09-910-411-1
Sequence 1, Application US/09910411
Patent No. US2002137054A1
GENERAL INFORMATION:
APPLICANT: Bergsma, Derek
APPLICANT: Fitzgerald, Laura
APPLICANT: Li, Xiaolong
APPLICANT: Michalovich, David
APPLICANT: Zhu, Yuan
TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
FILE REFERENCE: GP70655-2C1
CURRENT APPLICATION NUMBER: US/09/910,411
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 09/693,761
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/431,898
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapien
US-09-910-411-1

Alignment Scores:
Pred. No.: 8, 77e-138 Length: 1173
Score: 1308, 50 Matches: 252
Percent Similarity: 77, 52% Conservative: 48
Best Local Similarity: 65, 12% Mismatches: 84
Query Match: 64, 27% Indels: 3
Gaps: 3

US-10-626-398-10 (1-389) x US-09-910-411-1 (1-1173)

QY	5	AanSerThrlleAlaLeuThr--SerlleYsleSerleuThrPheleuNecSerleu	23
DB	13	AATGACACATCAATTTATCATAGCAGCTCGTGTACTTATGATTTATGCTTAA	72
QY	24	LeuAlaIleAlaIleMetleuGlyAenValValIleleuAlaPheIleValaPaag	43
DB	73	GTAAGCTTTGCTAATATGCTAGGAATGCTTGGCTATTGCTTTGGGGGACAA	132
QY	44	AenLeuArgHisArgSeranTyrrPhePheLeuAenLeuAlaIleAlaPhePheVal	63
DB	133	AACCTTAGCATCGAAGTAGTATTTTCTTAACCTTGCCATCTCTGATCTTTGG	192
QY	64	GlyAlaIleAlaIleProleuTyrlleProSerleuThrTyrrThrseryGlylys	83
DB	193	GCTGATCTCCATCTCTTGTATCATCCCTCACACCTCTTGCATGAGATTTTGAAG	252
QY	84	GlnAlaCyValPheThrleuIleThrAspTyrrleuCySerThrIleSerValTyraen	103
DB	253	GAATGCTGATTTTGGCTACTGACTATCTGTATGATACACATCTGTATTAAC	312
QY	104	IleValleuIleSerTyrrAsparGlyrglnSerValSerAsnAlaValTyrrYrarga	123
DB	313	ATTGCTCATATCAGCATATGATGATCCTGTCAGTCTCAATGCTGTCTTATATACT	372
QY	124	GlnHisSerGlyThrTrpIlyslleAlaThrGlnMetValAlaValTyrrIlePheSer	143
DB	373	CACACATCTGGGCTCTTGAAGATGTACTGATGCTGCGCTTTGGGGCTGGCCTTC	432
QY	144	MetThrAsnGlyProMetIleleuIleSerAspSerTrpGlnAsnSerThrThrglyys	163
DB	433	TTAGTGAATGGGCAATGATTTCTAGTTCAGACTCTTGAAGATGAAGTATGATGT	492
QY	164	GluProGlyPheleuTyrlsTyrrPheAlaIleuProThrSerleuGluPheleu	183

DB 493 GAACCTGATTTTTTCGAAATGATACATCTTGCCATCATCATTTCTTGAATTCGTG 552

QY 184 IleProIleleuLeuValAlaTyrrPheSerAlaHisIleTyrrTrpSerleuTrpIlyAsp 203

DB 553 ATCCAGATCATCTTATGCTTATTTCAACATGAATATTTATGAGCCTGTGGAAGCGT 612

QY 204 GlnTyLeuSerArgCysLeuSerHisProValleuProSerAspSerSerSerAsp 223

DB 613 GATCATCTGATGATGAGCAAGCAATCTCTGAGACTGACGTCTCTCTTCCAAATC 669

QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrleuProAlaArglyGlu 243

DB 670 TGTGAGACTCATTCAGAGTACATCTTCAAGAGATCTCTTCTGATCAGACAGA 729

QY 244 ThrThrAlaSerleuGlySerAspIlySerArgArglySerSerleuLeuProSerIle 263

DB 730 GTTCTGATCTTTTCATTCAGAGACAGAGAGAGATGTCATGTTTCTCA 789

QY 264 ArgAlaTyrrLeuAsnSeranValIleAlaSerIlyMetGlyPheleuSerHisSerAsp 283

DB 790 AGAACCAATGATATGCAATACATCTCTTCCAAATGGTCTCTTCCCATCATCAT 849

QY 284 SerleuAlaIleleuGlnGlnArgGlnHisIleGluLeuPheArgAlaArglyleuAlaIlys 303

DB 850 TCTGTAGCTCTTCAACAAAGGAAACATGTTGAACGCTTAGAGCCAGAGATTAGCCAAG 909

QY 304 SerleuAlaIleleuLeuAlaIlePheAlaIleCysTrpAlaProTyrrSerleuThrTrp 323

DB 910 TCACTGGCCATCTCTTAGGGGTTTGTGCTTGTGGCTCCCATATCTCTGTTCA 969

QY 324 ValIleTyrrSerPhePheProGluArgAenLeuThrIlySerThrTrpTyrrHisThrAla 343

DB 970 ATTGCTCTTCAATTTATTTCTCAGACAGACAGCTCCAAATCAGTTGATAGATTCGA 1029

QY 344 PheTrpLeuGlnTrpPheAsnSerPheValaenProPheleuTyrrProleuCyHisIlys 363

DB 1030 TTTTGGCTTCACTGATTCATCTTGTCAATCTCTTGTGATCATCTGATGTCACAA 1089

QY 364 ArgPheGlnIlyAlaPheleuTyrrleuProValArgArgIleSerThrPro--Pro 382

DB 1090 CGCTTCAAAAGGCTTCTTGAATAATTTGTATATAAAAGCAACCTTACATCACA 1149

QY 383 HisAsnArgSerIleSerThr 389

DB 1150 CACAGTGGTCAATCTTCT 1170

RESULT 6
US-09-875-076-13
Sequence 13, Application US/09875076
Publication No. US20030017528A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huang T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/09/875,076
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28

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; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-076-13

Alignment Scores:
Pred. No.:      8.77e-138      Length:      1173
Score:          1308.50        Matches:      252
Percent Similarity: 77.52%      Conservative: 48
Best Local Similarity: 65.12%      Mismatches: 84
Query Match:    64.27%         Indels:       3
DB:             10             Gaps:         3

US-10-626-398-10 (1-389) x US-09-875-076-13 (1-1173)
QY 5 AmsenrthrllealeuThr---SerileysileSerleuThrPheleuwerSerleu 23
DB 13 AATAGCAACAATCAATTTATCACTAAGCACTCGTGTACTTTTGAATTTTATGTCCTTA 72
QY 24 leualailealailemetleuGlyasnValValileleualaPheleValaspArg 43
DB 73 GTAGCTTTGCTAATATGCTAGGAATGCTTGGTCATTGATTTGCTTTGTGTGACAA 132
QY 44 AsnleuAIGHIAsrSerAsnTyrrPhePheleuAsnleualaileAlasPhePheVal 63
DB 133 AACCTTAACAACGAGTAATGTAATTTTCTTAATCTGGCCATCTGCACTTCTTTGTG 192
QY 64 GlyalailealaileProleuTyrrleProserSerleuThrTyrrThrsSerGlylys 83
DB 193 GGTGGAATCTCATCTCTTTGTGATCCCTCACAGCGTGTGGAATGGATTTGGAAAG 252
QY 84 GlnalaCyValPheTrpLeuIleThraPtyrLeuLeuCyThraIAserValTyrrAsn 103
DB 253 GAATCTGTGATTTTGGCTCACTGATCTATCTGTTATGACAGCATCTGTTATGAACT 312
QY 104 lleValleuIleSerTyrrAspArgTyrrGlnSerValSerAsnAlaValTrpTyrrAla 123
DB 313 ATTGCCCATCAGCTATGATGATGATACCGTCAAGTCTCAATGCTGTGCTTATGAACT 372
QY 124 GlnHisSerGlyThrTrpLeuIlealaThrglnmetValAlaValTrpIlePheSerPhe 143
DB 373 CAACATCTGGGGCTTGAAGATTGTACTGATGGGCGGTTGGGTGGCTGGCTTTC 432

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QY 144 MetThrAsnGlyProMetIleleuIleSerAspSerTrpGlnAsnSerThrThrgluCys 163
DB 433 TTAGTGAATGGGCCAATATATTCTAGTTTCAAGGCTTTGGAAGATGAAGTGTGAATGT 492
QY 164 GluProGlyPheLeuValyTrpTyrrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
DB 493 GAACCTGATTTTTCGGAATGGACATCTCTGGCATCATCTTCTTGAATTTGCTG 552
QY 184 IleProIleleuLeuValAlaTyrrPheSerAlaHisIleTyrrTrpSerleuTrpIlyAsp 203
DB 553 ATCCAGATCATCTTAGTGGCTTATTTCAACATGAATATTTATGAGCCTGTGAAAGCT 612
QY 204 GluIlySerSerArgCysLeuSerHisProValleuProSerAspSerSerSerAsp 223
DB 613 GATCATCTCAGAGGTGCAAGCATCTGAGACTGACTGCT---GTCCTTCCAACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArglyGlu 243
DB 670 TGTGACACTCATTCAGAGTGAAGTAACTTCAAGAGATCTCTTCTGCAATGACAGA 729
QY 244 ThrThrAlaSerleuGlySerAspIlySerArgIlySerSerSerleuLeuProSerile 263
DB 730 GTTCTGCAATCTTTCATTCAGAGACAGAGAGAGAAAGATGATCTATGTTCTTCA 789
QY 264 ArgAlaTyrrIlyAsnSerAsnValIleAlaSerIlyMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGAATAGCAATATCAATGCTTCCAAATGGTCTCTCCCAATCAGAT 849
QY 284 SerleuAlaLeuGlnGlnArgGlnHisIleGluLeuPheAlaArgIlyLeuAlaIlys 303
DB 850 TCTGTAGCTCTTCCAAAGGAACATGTTGAACGCTTAGAGCCAGAGATTTACCAAG 909
QY 304 SerleuAlaIleleuLeuAlaAlaPheAlaIleCysTrpAlaProTyrrSerleuThr 323
DB 910 TCACGTGGCATTCCTTCTTAGGGGTTTCTGTTCTGCTGCTGCTATCTCTGTTCA 969
QY 324 ValIleTyrrSerPhePheProGlnArgAsnleuThryIlySerThrTrpTyrrHisThra 343
DB 970 ATTGCCCTTCAATTTATTTCCAGCAACAGGCTCTAATATGTTGGATGAAATGGA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheleuTyrrProleuCyHisIlys 363
DB 1030 TTTTGGCTTCAGTGGTGAATTCCTTGTGCAATCTCTTTGTATCCATTTGTGTACAA 1089
QY 364 ArgPheGlnIlyAlaPheLeuIlyIleuProValArgArgGlnSerThrPro---Pro 382
DB 1090 CGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATAAAAAGCAACCTCTACATCACAA 1149
QY 383 HisAsnArgSerIleSerThr 389
DB 1150 CACAGTCGTCAGTATCTTCT 1170

RESULT 7
US-09-876-252-13
; Sequence 13, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinema, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Rece
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496

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:	PRIOR FILLING DATE:	1998-10-13
:	PRIOR APPLICATION NUMBER:	60/110,066C
:	PRIOR FILING DATE:	1998-11-27
:	PRIOR APPLICATION NUMBER:	60/120,416
:	PRIOR FILING DATE:	1999-02-16
:	PRIOR APPLICATION NUMBER:	60/121,852Z
:	PRIOR FILING DATE:	1999-02-26
:	PRIOR APPLICATION NUMBER:	60/109,213
:	PRIOR FILING DATE:	1998-11-20
:	PRIOR APPLICATION NUMBER:	60/123,944A
:	PRIOR FILING DATE:	1999-03-12
:	PRIOR APPLICATION NUMBER:	60/123,945S
:	PRIOR FILING DATE:	1999-03-12
:	PRIOR APPLICATION NUMBER:	60/123,946B
:	PRIOR FILING DATE:	1999-03-12
:	PRIOR APPLICATION NUMBER:	60/123,949A
:	PRIOR FILING DATE:	1999-03-12
:	PRIOR APPLICATION NUMBER:	60/152,524A
:	PRIOR FILING DATE:	1999-09-03
:	PRIOR APPLICATION NUMBER:	60/151,114A
:	PRIOR FILING DATE:	1999-08-27
:	PRIOR APPLICATION NUMBER:	60/108,029P
:	PRIOR FILING DATE:	1998-11-12
:	PRIOR APPLICATION NUMBER:	60/136,436E
:	PRIOR FILING DATE:	1999-05-28
:	PRIOR APPLICATION NUMBER:	60/136,439P
:	PRIOR FILING DATE:	1999-05-28
:	PRIOR APPLICATION NUMBER:	60/136,567F
:	PRIOR FILING DATE:	1999-05-28
:	PRIOR APPLICATION NUMBER:	60/137,127T
:	PRIOR FILING DATE:	1999-05-28
:	PRIOR APPLICATION NUMBER:	60/137,131J
:	PRIOR FILING DATE:	1999-05-28
:	PRIOR APPLICATION NUMBER:	60/141,448B
:	PRIOR FILING DATE:	1999-06-29
:	PRIOR APPLICATION NUMBER:	60/136,437T
:	PRIOR FILING DATE:	1999-05-28
:	PRIOR APPLICATION NUMBER:	60/156,555S
:	PRIOR FILING DATE:	1999-09-29
:	PRIOR APPLICATION NUMBER:	60/156,634A
:	PRIOR FILING DATE:	1999-09-29
:	PRIOR APPLICATION NUMBER:	60/156,653K
:	PRIOR FILING DATE:	1999-09-29
:	PRIOR APPLICATION NUMBER:	60/157,280I
:	PRIOR FILING DATE:	1999-10-01
:	PRIOR APPLICATION NUMBER:	60/157,294A
:	PRIOR FILING DATE:	1999-10-01
:	PRIOR APPLICATION NUMBER:	60/157,291I
:	PRIOR FILING DATE:	1999-10-01
:	PRIOR APPLICATION NUMBER:	60/157,282Z
:	PRIOR FILING DATE:	1999-10-01
:	PRIOR APPLICATION NUMBER:	60/156,633K
:	PRIOR FILING DATE:	1999-09-29
:	NUMBER OF SEQ ID NOS:	146
:	SOFTWARE:	PatentIn version 3.0
:	SEQ ID NO 13	
:	LENGTH:	1173
:	TYPE:	DNA
:	ORGANISM:	Homo sapiens
:	US-09-876-252-13	
 Alignment Scores:		
:	Pred. No.:	8.77e-138
:	Scores:	1308.50
:	Percent Similarity:	77.52%
:	Best Local Similarity:	65.12%
:	Query Match:	64.27%
:	DB:	10

US-10-626-398-10	(1-389)	x	US-09-876-252-13	(1-1173)
QY	5	AsnSerThrIleAlaLeuThr--SerIleLysIleSerLeuThrPheLeuMetSerLeu	23	
Db	13	AATAGGCAACATCATTTATATCACTAAGCACTGCTGTTACTTATAGCATTTTATATGCTTTA	72	
QY	24	LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg	43	
Db	73	GTACCTTTGGTAAATAGCTAAGAAATGCTTTGGTCATTTCATTAGCTTTGGTGTGACAA	132	
QY	44	AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal	63	
Db	133	AACCTTGACATCGAAGTAGTATTTTTTTCTTAACCTTGAGCACTCTGACTTCTTTGTG	192	
QY	64	GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys	83	
Db	193	GGTGTGATCTTCATTTCTTTGTATCATCCCTCACACGGCTTGCAATGGATTTTGGAAAG	252	
QY	84	GlnAlaCysValPheTrpPheIleThrAspTyrIleLeuCysTrpAlaSerValTyrAsn	103	
Db	253	GAAATCTGTGTATTTTGGCTCACACACATCTGTATGTAAAGCATCTGTATATAC	312	
QY	104	IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla	123	
Db	313	ATTGTCTTCATCACTATGATATCACTGTCACTGCTCAATGCTGTGTCTTATAGAACT	372	
QY	124	GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe	143	
Db	373	CAACATATCTGGGGCTTGAAGATTTGTTAACTGTAGTGGTGGCTGGCTTC	432	
QY	144	MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThiGlyLys	163	
Db	433	TTACTGATGGGCCAAATGATTCCTGATTCTCAAGCTCTTGAAGATGAAGTAGAAGT	492	
QY	164	GlnProGlyPheLeuLysTrpTyrPheAlaLeuProThrSerLeuGlnPheLeu	183	
Db	493	GAACTGGATTTTTTGGAAATGGATACCTTCCCATCAATCATCTTGGAAATTCGAG	552	
QY	184	IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg	203	
Db	553	ATCCACAGCATCTTATGTCGTTATTTCAACATGAATATTATATGAGGCTGTGGAAGGT	612	
QY	204	GlnLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp	223	
Db	613	GATCATCTGAGTAGTGCCAAAGCCATCTGAGTCACTGCT--GTCCTTCCAAACATC	669	
QY	224	HisGlyIleSerCysArgGlnAspProAspSerArgAlaThrIleuProAlaArgLysIleu	243	
Db	670	TGTGGAACTCATTTCAAGAGTAGACTATCTTCAAGAGATCTTTTGTGATCGACAA	729	
QY	244	ThrThrIleSerLeuGlySerAspLysSerArgTyrGlyLysSerSerLeuLeuProSerIle	263	
Db	730	GTTCCCTGCATCTTTCATTCAGAGACACAGAGAAAGTAGTATCTCATGTTTCTTCA	789	
QY	264	ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp	283	
Db	790	AGAACCAAGATGAATACCAATACATATGCTTCCAAATAGGGTCTCTTCCCAATACAGAT	849	
QY	284	SerLeuAlaLeuGlnGlnArgGlnHisIleGlnLeuPheArgAlaArgLysLeuAlaLys	303	
Db	850	TCTGTACTCTTCCAAAGGAAAGCAATGTTGATCTGTAAAGCAGAGATTTAGGCCAAG	909	
QY	304	SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr	323	
Db	910	TCACTGGCCATCTCTTAAAGGGTTTTTGGCTGTGCTGGGCTCCATATCTCTGTTCAC	969	
QY	324	ValIleTyrSerPhePheProGlyuArgAsnLeuThrLysSerThrTyrThrAla	343	
Db	970	ATTGTCTTTCATTTTATTCCTCGCAACAGGCTCTTAATACAGTTTGGTATAGAAATGCA	1029	
QY	344	PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys	363	
Db	1030	TTTGGCTCAGTGGTCAATCTCTTGTGCATCTCTTTGGTATCCATGTGTGCACAG	1089	


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/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-626-398-10
US-10-626-398-10 (1-389) x US-10-626-398-10 (1-1173)

Alignment Scores:
Pred. No.: 8,77e-138 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64,27% Indels: 3
DB: 15 Gaps: 3

US-10-626-398-10 (1-389) x US-10-626-398-10 (1-1173)
QY 5 AaenSerThrIleAlaLeuThr---SerIleYsIleSerLeuThrPheLeuMetSerLeu 23
DB 13 AATAGCAATCAATTAATTAATCACTAGCACTGCTGTTAGCAATTTTATGCTCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTTGCTAATAGTGAAGAAAGCTTGCTGCTTTAGCTTTTGCTGAGCAAA 132
QY 44 AaenLeuArgHisArgSerAsnIlePhePheLeuAsnLeuAlaIleAlaAspPhePheVal 63
DB 133 AACCTTAGCATGAGTACGATGATTTTCTTAACTGGCACTCTGCTCTTTGTC 192
QY 64 GlyAlaIleAlaIlePheLeuThrIlePheSerSerLeuThrIlePheSerGlyLeu 83
DB 193 GGTGTGCTCTCCTTCTTGTACATCCCTCACACGCTGTTCGAAATGGATTGGAAAG 252
QY 84 GluAlaCysValPheTrpLeuIlePheAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
DB 253 GAATATCGTATATTGGCTCAGTACGATCTGTTAGTACAGCATCTGATATTAAC 312
QY 104 IleValIleLeuSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTyrArgAla 123
DB 313 ATGTCTCTCATGAGCTATGATCATCTGCTCAATGCTGCTGCTTATAGAACT 372
QY 124 GluHisSerGlyThrTrpIleValIleAlaThrGlnMetValAlaValTyrIlePheSerPhe 143
DB 373 CAACATACCTGGGCTCTTGAAGATGTTACTGATGATGGCCGCTGGGGCTGGCCCTTC 432
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTyrPheIleAsnSerThrGluCys 163
DB 433 TTAGTGAATGGCCAAAGATTTAGTTTCAAGAGCTTGGAAAGATGAGTGAATGT 492
QY 164 GluProGlyPheLeuValTyrTyrPheAlaLeuProThrSerLeuGluPheLeu 183
DB 493 GAACCTGATTTTTCGAAATGATGATCTTCCATCATCATCATCTTGAATTCGTG 552
QY 184 IleProIleLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTyrValArg 203
DB 553 ATCCCATCTATCTTATGCTTATTTTCAACATGAATTTTATGAGACCTGTGAGACGT 612
QY 204 GluValLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 613 GATCATCTAGTAGTCCAAAGCATCTGAGATGAGTCT---GTCTCTTCCAAATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrIleProAlaGlyValGlu 243
DB 670 TGTGCACTCATCTCAAGAGTAGACTATCTTCAAGAGATCTCTTCTGATGACAGAA 729
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QY 244 ThrThrAlaSerLeuGlySerAspIleValArgValArgValSerSerLeuProSerIle 263
DB 730 GTTCCGCAATCTCTTATTCATGAGAGACAGAGAGAGAGAGTGTCTCATGTTTCTCA 789
QY 264 ArgAlaTyrIleAsnSerAsnValIleAlaSerIleMetCysPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGAATGATGATATGATGATGATGATGATGATGATGATGATGATGAT 849
QY 284 SerLeuAlaLeuGlnGlnArgGlnHisIleGlnLeuPheArgValArgValSerLeuAlaVal 303
DB 850 TGTGTGCTCTTACCAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 909
QY 304 SerLeuAlaIleLeuValAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
DB 910 TCATGCGCATTTCTCTTAGGAGGTTTTCGCTGTTGCTGCGGCTCATATTTCTGTTGACA 969
QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrIleYsSerThrTyrTyrHisThrAla 343
DB 970 ATGTGCTTTCATTTATTTCTCAGCAACAGTCTTAATCAATGATTTGATAGAAATTCGA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuThrProLeuCysHisIleVal 363
DB 1030 TTTTGGCTTCAGGTTCATTTCTTGTCAATCTCTTGTGATTCATTTGTGATTCATTCACAG 1089
QY 364 ArgPheGlnValAlaPheLeuValIleLeuProValArgGlnSerThrPro---Pro 382
DB 1090 CGCTTTCAAAAGAGCTTTCTTGAAATATTTTGTGATTAATAAAGCACTCATCATCA 1149
QY 383 HisAsnArgSerIleSerThr 389
DB 1150 CACATGCGTCAATCTTCT 1170

RESULT 10
US-10-354-769-1
/ Sequence 1, Application US/10354769
/ Publication No. US20030149242A1
/ GENERAL INFORMATION:
/ APPLICANT: Pfizer Inc.
/ APPLICANT: Peter, Beate
/ TITLE OF INVENTION: NOVEL POLYPEPTIDE
/ FILE REFERENCE: P0103738
/ CURRENT APPLICATION NUMBER: US/10/354,769
/ PRIOR FILING DATE: 2003-01-30
/ PRIOR APPLICATION NUMBER: US 09/698,801
/ PRIOR FILING DATE: 2000-10-27
/ PRIOR APPLICATION NUMBER: US 60/211,243
/ PRIOR FILING DATE: 2000-06-14
/ PRIOR APPLICATION NUMBER: GB 9925641.4
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: GB 0009973.9
/ PRIOR FILING DATE: 2000-04-20
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-354-769-1

Alignment Scores:
Pred. No.: 8,77e-138 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64,27% Indels: 3
DB: 15 Gaps: 3

US-10-626-398-10 (1-389) x US-10-354-769-1 (1-1173)
QY 5 AaenSerThrIleAlaLeuThr---SerIleYsIleSerLeuThrPheLeuMetSerLeu 23
DB 13 AATAGCAATCAATTAATTAATCACTAGCACTGCTGTTAGCAATTTTATGCTCTTA 72
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Db      253  GAAATCTGTGATTTTGGCTCACTACAGACTATCTGTTATGTACGCACTCTGTATATAC 312
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Qy      104  ILevalLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTyrArgAla 123
               |||
Db      313  ATTGCTCATCAGCTATGATGATGATACCGTCAGCTCAAAATGCTGTCTTTATAGACT 372
               |||
Qy      124  GlnHsSerGlyThrTPrpYsIleAlaThrGlnMetValAlaValTyrIlePheSerPhe 143
               |||
Db      373  CAACACTACTGGGGCTTGTAGAGATTGTTACTCTGAGAGTGGCGGTTTGGGTCTGGCCCTTC 432
               |||
Qy      144  MetThrAsnGlyProMetIleLeuIleSerAspSerTPrpGlnAsnSerThrThiGluYs 163
               |||
Db      433  TTAGCGAATGGCCCAATATCTTACTGTTTCAAGACTTTGGAAGAGAAAGTAGTAGT 492
               |||
Qy      164  GluProGlyPheLeuYsIleTPrpTyrPheAlaLeuProThrSerLeuGluPheLeu 183
               |||
Db      493  GAACCTGGATTTTTTGGGAATGGTAACATCCCTGGCATCACATCATCTTGGAAATCGTG 552
               |||
Qy      184  IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTPrpSerLeuTPrpYsArg 203
               |||
Db      553  ATCCACAGACTCTTAGTCGCTTATTCAACATGAAATATTATTAGGACCTGTGGAAACGT 612
               |||
Qy      204  GluYsIleuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerp 223
               |||
Db      613  GATCATCTCAGAGAGGTGCCAAAGCCATCTGGACGACTGCT--GTCTCTTCAACATC 669
               |||
Qy      224  HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgYsIle 243
               |||
Db      670  TGTGGACACTCATTCAGACGTAAGACTATCTTCAGAGAAATCTCTTCTGCATCCAGAGA 729
               |||
Qy      244  ThrThrAlaSerLeuGlySerAspYsSerArgArgYsSerSerLeuLeuProSerIle 263
               |||
Db      730  GTTCCCTGCATCTTTCATTCAGAGAGACAGAGAGAAAGAGTCTCATGTTTCTCTCA 789
               |||
Qy      264  ArgAlaTyrYsAsnSerAsnValIleAlaSerYsMetGlyPheLeuSerHisSerAsp 283
               |||
Db      790  AGAACCAAGATGAATGAACATAACAATTCCTTCCAAATGGGTTCTTCTCCAAATCAGAT 849
               |||
Qy      284  SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgYsLeuAlaYs 303
               |||
Db      850  TCTGTAGCTCTTCACCAAGGAGAACATTTGAATCGCTTAAGCCAGAGATTAACCCAG 909
               |||
Qy      304  SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTPrpAlaProTyrSerLeuThr 323
               |||
Db      910  TCACGTGGCATCTTCTTAGGGGTTTTCGTGTGCTGGGCTCAATATCTCTGTTCACA 969
               |||
Qy      324  ValIleTyrSerPhePheProGluArgAsnLeuThrYsSerThrTPrpYHisThrAla 343
               |||
Db      970  ATTGTCTTTCAATTTATTTCTCTCAGCAACAGGTCCTAATATCAGTTGTGTATGAAATGCA 1029
               |||
Qy      344  PheTPrpLeuGlnTPrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisYs 363
               |||
Db      1030  TTTTGGCTTCAGTGGTCAATTCCTTTTCAATTCCTTTGTGATCATTGTCACAG 1089
               |||
Qy      364  ArgPheGlnYsAlaPheLeuYsIleLeuProValaArgGlnSerThrPro--Pro 382
               |||
Db      1090  CGCTTTCAAAAGGCTTCTTGAAATAATTTGTATATAAAAAAGCAACCTTCACATCAACA 1149
               |||
Qy      383  HisAsnArgSerIleSerThr 389
               |||
Db      1150  CACAGTCCGTCAGTATCTTCT 1170
               |||

RESULT 12
US-10-417-820A-13
; Sequence 13, Application US/10417820A
; Publication No. US20030229216a1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.

```

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: TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
: FILE OF INVENTION: Receptors
: FILE REFERENCE: 7.US28.CON
: CURRENT APPLICATION NUMBER: US/10/417,820A
: CURRENT FILING DATE: 2003-04-16
: PRIOR APPLICATION NUMBER: 09/416,760
: PRIOR FILING DATE: 1999-10-12
: PRIOR APPLICATION NUMBER: 09/170,496
: PRIOR FILING DATE: 1998-10-13
: PRIOR APPLICATION NUMBER: 60/110,060
: PRIOR FILING DATE: 1998-11-27
: PRIOR APPLICATION NUMBER: 60/120,416
: PRIOR FILING DATE: 1999-02-16
: PRIOR APPLICATION NUMBER: 60/121,852
: PRIOR FILING DATE: 1999-02-26
: PRIOR APPLICATION NUMBER: 60/109,213
: PRIOR FILING DATE: 1998-11-20
: PRIOR APPLICATION NUMBER: 60/123,944
: PRIOR FILING DATE: 1999-03-12
: PRIOR APPLICATION NUMBER: 60/123,945
: PRIOR FILING DATE: 1999-03-12
: PRIOR APPLICATION NUMBER: 60/123,948
: PRIOR FILING DATE: 1999-03-12
: PRIOR APPLICATION NUMBER: 60/123,951
: PRIOR FILING DATE: 1999-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 155
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 13
: LENGTH: 1173
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-417-820A-13

Alignment Scores:
Pred. No.:      8,77e-138      Length:      1173
Score:          1308.50       Matches:     252
Percent Similarity: 77.52%    Conservative: 48
Best Local Similarity: 65.12% Mismatches:   84
Query Match:     64.27%      Indels:      3
DB:              17          Gaps:         3
US-10-626-398-10 (1-389) x US-10-417-820A-13 (1-1173)
QY      5 AenSerThrIleAlaLeuThr--SerIleYsIleSerLeuThrPheLeuMetSerLeu 23
DB      13 AATAGCACAATCAATTATACACTAGCAAGCACTCGTGTAATTGACATTTTATATGCTCTTA 72
QY      24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
DB      73 GAGAGCTTTGGCTATATAGCTAGAGAATGGCTTGTCATTTTAGCTTTTGGTGACAA 132
QY      44 AsnLeuAlaGHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
DB      133 AACCTTAACACATCGAAGTAGTAATTTTCTTAACCTTGGCCATCTGACATTCCTATG 192
QY      64 GAlaAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpHisSerGlyLys 83
DB      193 GGTGTCATCTCCATTCCTTTTGACATCCCTCACACGCTGTGGATGGAGATTTGGAAAG 252
QY      84 GAlaAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
DB      253 GAAATCTGTGATTTTGGCTCACTACTGACATCTGATCTGATAGACATCTGATATTAAC 312
QY      104 IleValIleuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123
DB      313 ATTGCTCATCAAGCTATGATGCAATCACTGATAGCTCAAAAGCTGTGCTTATTAAC 372
QY      124 GlnHisSerGlyThrTrpIleAlaIleAlaTrgIleMetValAlaValTrpIlePheSerPhe 143
DB      373 CAACATCACTGGGGCTTGAAGATGTACTCGATGATGGGCCGCTTTGGGCTGCGCTTC 432
QY      144 MetTrpAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrgIuGly 163

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Db 433 TTAGTGAAGGGCCATGATGTTCTAGTTTCAGAGTCTTGAGAGATGAGATGAGTGAATGT 492
Qy 164 GIUPROG1YPheLeuLysTrpTyRheAlaLeuProThSerLeuLeuGluPheLeu 183
Db 493 GAACCTGGATTTTTCGGAATGGTACATCTTCCTGACATCATCTTCTTGGAATTCGG 552
Qy 184 ILeProIleLeuLeuValAlaTyRheSerAlaHisIleTyRTrpSerLeuTrpLysArg 203
Db 553 ATCCAGATCATCTTATGCTGCTTATTTCAACATGAAATTTATTTGAGCGCTGGAGAGCT 612
Qy 204 GIULYSLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGGAGCCAAAGCCATCTGAGCATGACTGCT---GTCCTTCCAACATC 669
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProLalaArgLysGlu 243
Db 670 TGTGACACTCATCTCAGAGTAGACTATCTTCAAGAGATCTCTTCTTCGACATCGACAGA 729
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
Db 730 GTTCCGATCCTTTTCATTCAGAGAGACAGAGAGAAAGTAGTCTCATGTTTTCCTCA 789
Qy 264 ARGAlaTyRlyAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATGAAATAGCAATACAAATTCCTCCAAATGGTCTCTCCCAATCAGAT 849
Qy 284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
Db 850 TCTGTAGCTCTTCACCAAGGAGACATGTTGAATCTTAGAGCCAGAGATTAAGCCANG 909
Qy 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTySerLeuThr 323
Db 910 TCACGTGGCATCTCTTACGGGTTTGTGCTGTGGTGGCTCCATATCTCGTTGACACA 969
Qy 324 ValIleTySerPhePheProGluArgAsnLeuThrLysSerThrTrpTyHisThrAla 343
Db 970 ATTGTCCTTTCATTTTATCTTCACAGACAGAGCTCTAAATCAGTTTGATGAAATGCA 1029
Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyRProLeuCysHisLys 363
Db 1030 TTTTGGCTTCAGTGGTCAATCTTGTCAATCTCTTTGTATCCATGTCGTACANG 1089
Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgLysSerThrPro---Pro 382
Db 1090 CCTTTCAAAAGGCTTTCTGAAAATATTTGTGATAAAAGCAACCTCTACATCACA 1149
Qy 383 HisAsnArgSerIleSerThr 389
Db 1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 13
US-10-349-253A-1
; Sequence 1, Application US/10349253A
; Publication No. US20040043393A1
; GENERAL INFORMATION:
; APPLICANT: Aubart, Kelly
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Graybill, Todd
; APPLICANT: Li, Xiaolong
; APPLICANT: Michalovich, David
; APPLICANT: Morrow, Dwight
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C2
; CURRENT APPLICATION NUMBER: US/10/349,253A
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/910,411
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
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; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-349-253A-1

Alignment Scores:
Pred. No.: 8.77e-138 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
Dels: 18 Gaps: 3

US-10-626-398-10 (1-389) x US-10-349-253A-1 (1-1173)
Qy 5 AenSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCAATCAATCAATTTATCTACTAGACACTGCTGTTACTTTAGCATTTTATGCTCTTA 72
Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTGCTATATATCTAGAAATGCTTGGTCAATTTAGCTTTGCTGGTGACANA 132
Qy 44 AsnLeuAlaGHisArgSerAsnTyRhePheLeuAsnLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTACACATCGAAGTAGTATTTTCTTAATCTGGCCATCTCGACTTCCTTGTG 192
Qy 64 GIYAlaIleAlaIleProLeuTyRLeProSerSerLeuThrTyRTrpThrSerGlyLys 83
Db 133 GGTGTGATCTCTCATCTTCTTTGATCTTCCACACAGCTGTTGGAATGGATTTGGAANG 252
Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyRLeuLeuCysThrAlaSerValTyRAsn 103
Db 253 GAAATCTGTATTTTGTGCTCACTGACTGATCTGTTATGACAGCATCTGATATATAC 312
Qy 104 ILeValLeuIleSerTyRAspArgTyRLeuSerValSerAsnAlaValTyRArgAla 123
Db 313 ATTGCTTCATCAGCTATGATGATGATGATCTGATGATCTGATGATGATGATGATGAT 372
Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
Db 373 CAACATCTGGGCTTGAAGATTTCTTACTGATGATGATGATGATGATGATGATGATGAT 432
Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGlyCys 163
Db 433 TTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAAGATGAGTAGTGAATGT 492
Qy 164 GIUPROG1YPheLeuLysTrpTyRheAlaLeuProThSerLeuLeuGluPheLeu 183
Db 493 GAACCTGGATTTTTCGGAATGGTACATCTTCCTGACATCATCTTCTTGGAATTCGG 552
Qy 184 ILeProIleLeuLeuValAlaTyRheSerAlaHisIleTyRTrpSerLeuTrpLysArg 203
Db 553 ATCCAGATCATCTTATGCTGCTTATTTCAACATGAAATTTATTTGAGCGCTGGAGAGCT 612
Qy 204 GIULYSLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGGAGCCAAAGCCATCTGAGCATGACTGCT---GTCCTTCCAACATC 669
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProLalaArgLysGlu 243
Db 670 TGTGACACTCATCTCAGAGTAGACTATCTTCAAGAGATCTCTTCTTCGACATCGACAGA 729
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
Db 730 GTTCCGATCCTTTTCATTCAGAGAGACAGAGAGAAAGTAGTCTCATGTTTTCCTCA 789
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QY 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGATGACATATGCTTCCAAATGGGCTTCCTTCCCAATCAGAT 849
QY 284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
DB 850 TCTGTAGCTCTTACCAAGGGAACATGTTGAACCTGTTAGACCCAGGAAATTAGCCAA 909
QY 304 SerLeuAlaIleLeuLeuAlaIlePheAlaIleCysThrAlaProTyrSerLeuThrTrp 323
DB 910 TCACTGGCCATCTCTTAGGGGTTTGTGCTTTGCTGGGCTCCATATCTCTGTTCA 969
QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343
DB 970 ATGTGCTTATTTATTTATTCAGCAACAGTCCATAATCAGTTGGTATGAATTGCA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
DB 1030 TTTTGGCTTCAGGCTTCATTCCTTTGTCATCTTTTGTATCCATGTGTCAAG 1089
QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgLysSerThrPro---Pro 382
DB 1090 CGCTTTCACAAAGGCTTCTTGAAATAATTTTGTATATAAAGCAACCTTACATCA 1149
QY 383 HisAsnArgSerIleSerThr 389
DB 1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 14
US-10-723-955-13
Sequence 13, Application US/10723955
Publication No. US20040110238A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmer, Derek T.
APPLICANT: Lin, I-Hsin
APPLICANT: Liao, Chen W.
APPLICANT: Lehman-Brulnsma, Karin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Dang, Huang T.
APPLICANT: Chen, Kuoping
APPLICANT: Gore, Martin
APPLICANT: White, Carol
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: 7.UG29.CON
CURRENT APPLICATION NUMBER: US/10/723,955
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 10/417,820
PRIOR FILING DATE: 2003-4-16
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.2
SEQ ID NO 13
LENGTH: 1173
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TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-955-13

Alignment Scores:
Pred. No.: 8, 77e-138
Score: 1308.50
Percent Similarity: 77.52%
Best Local Similarity: 65.12%
Query Match: 64.27%
DB: 19 Gaps: 3

US-10-626-398-10 (1-389) x US-10-723-955-13 (1-1173)

QY 5 AsnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
DB 13 AATGACACATCAATTTATCTACAGCACTCGGTACTTACATTTTATGCTTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTGCTATATAGCTAGGAATGCTTGGTCACTTTAGCTTTGTGTGACAA 132
QY 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
DB 133 AACCTTAGACATCGAAGTAGTATTTTCTTAACTGGCCATCTCTGCTTTGTG 192
QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpHisSerGlyLys 83
DB 193 GGTGATCTCCATCTTGTGATACCTCCACACGCTGTCGAATGGATTTGGAAAG 252
QY 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
DB 253 GAATGCTGTATTTTGGCTACTGACTGACTATCTTATGATACATCTGTATTAAC 312
QY 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTyrAla 123
DB 313 ATGTCTCATCAGCATGATGATCATCTGCTGAGTCAAACTGCTGTATTAAGACT 372
QY 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
DB 373 CAACATCTGGGCTTGAAGATGTTACTCTGATGATGCGCTTGGGGCTGGCTTC 432
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGlyCys 163
DB 433 TTAGTAATGGGCGCATGATTTCTAGTTCAAGTCTTGAAGATGAAGTATGATGT 492
QY 164 GluProGlyPheLeuLysIleTyrPheAlaLeuProThrSerLeuGluPheLeu 183
DB 493 GAACCTGGATTTTTCGGAATGATCATCTTGCATGACATCTTGGAAATTCGTG 552
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
DB 553 ATCCAGTATCTTATGCTTATTTTCAACATGAATAATTAATGAGCCGTGAAAGCGT 612
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 613 GATCATCTCAGTAGGCGCAAGCCATCTGAGTACGTGCT---GTCTTTTCAACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGln 243
DB 670 TGTGACACATCTTACAGAGTAGACTATCTTCAAGAGAGATCTTCTCTGATGACAGAA 729
QY 244 ThrThrAlaSerLeuLysSerAspLysSerArgLysSerSerLeuLeuProSerIle 263
DB 730 GTTCTGCACTCTTTCATTCAGAGACAGAGAGAAAGTAGTCAATGTTTCTCTCA 789
QY 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGATGACATATGCTTCCAAATGGGCTTCCTTCCCAATCAGAT 849
QY 284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
DB 850 TCTGTAGCTCTTACCAAGGGAACATGTTGAACCTGTTAGACCCAGGAAATTAGCCAA 909
```

Qy 304 SerLeuAlaIleLeuLeuAlaIleAphaeAlaIleCystrPaIaProTySerLeuThr 323
Db 910 TCACGGCCATCTCTTACGGGTTTTCGTGTTGGGCTCCATATCTCTGTTCACA 969
Qy 324 ValIleTySerPhePheProGluArganLeuThrIleSerThrTrpTyriIsthAla 343
Db 970 ATTGCTTCCTTCAATTTATCTTCACGACAGGCTCTTAATCAGTTGGTATGAATTGCA 1029
Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValaAnProPheLeuTyProleuCyshiIlyS 363
Db 1030 TTTTGCTTCACGTGTTCAATTCCTTTCGCAATCTCTTTGTATCCATGTGTCAANG 1089
Qy 364 ArgPheGlnIlyAlaPheLeuIlyIleuProValArgArgGlnSerThrPro--Pro 382
Db 1090 CCCTTTCAAAAGGCTTCTTGAATAATTTGTATGAATAAAGCAACCTCACATCACAA 1149
Qy 383 HisAenArgSerIleSerThr 389
Db 1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 15

US-10-782-596-13

Sequence 13, Application US/10782596

Publication No. US20040137509A1

GENERAL INFORMATION:

APPLICANT: Chen, Ruoping

APPLICANT: Dang, Huang T.

APPLICANT: Liaw, Chen W.

APPLICANT: Lin, I-Lin

TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors

FILE REFERENCE: AREN0050

CURRENT APPLICATION NUMBER: US/10/782,596

CURRENT FILING DATE: 2004-02-19

PRIOR APPLICATION NUMBER: US/09/875,076

PRIOR FILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: 09/417,044

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/121,851

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/123,946

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,949

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/136,436

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,437

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,439

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,567

PRIOR FILING DATE: 1999-05-28

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 74

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13

LENGTH: 1173

TYPE: DNA

ORGANISM: Homo sapiens

US-10-782-596-13

Alignment Scores:

Pred. No.:	8, 77e-138	Length:	1173
Score:	1308.50	Matches:	252
Percent Similarity:	77.52%	Conservative:	48
Best Local Similarity:	65.12%	Mismatches:	84
Query Match:	64.27%	Indels:	3
DB:	19	Gaps:	3

US-10-626-398-10 (1-389) x US-10-782-596-13 (1-1173)

Qy 5 AenSerThrIleAlaLeuThr--SerIleIlyIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATACCAATCAATTAATTAATCACTAGACACTCGTGTACTTATGATTTTATGTCCTTA 72
Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleAlaParg 43
Db 73 GTAGCTTTGCTATATATCTAGAAATCTTTGGTCATTATTAAGCTTTGTGTGACAA 132
Qy 44 AenLeuArgHisArgSerAsnTyrrPhePheLeuAenLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTAGACATCGAAGATGATTTTCTTAATCTTGCCATCTGACCTCTTTGG 192
Qy 64 GlyAlaIleAlaIleProLeuTyrrIleProSerSerLeuThrTyrrThrSerGly 83
Db 193 GGTGTGATCTCCATTCCTTTGACATCCCTCACAGCTGTTGGAATGGATTTGGAAAG 252
Qy 84 GlnAlaCyValPheTrpLeuIleThrAspTyrrLeuLeuCyThrAlaSerValTyrr 103
Db 293 GAAATCTGTATTTTGGCTACTACTATCTGTATGTATGACGATCTGTATATAC 312
Qy 104 IleValIleuIleSerTyrrAspArgTyrrGlnSerValSerAsnAlaValTyrrArgAla 123
Db 313 ATTGCTCATCAGCTATGATGATGATCCTGTCAGTCTCAAAAGCTGTCTTATAGACT 372
Qy 124 GlnHisSerGlyThrTrpIlyIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
Db 373 CAACATACCTGGGCTTGAAGATGTACTGATGAGTGCCGTTGGGTGCTGACCTTC 432
Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrArgGly 163
Db 433 TTAGTGAATGGCCATATATCTAGTTTCAGAGCTTGAAGATGAAGTGTGAAT 492
Qy 164 GlnProGlyPheLeuIlySerTrpTyrrPheAlaLeuProThrSerLeuGlnPheLeu 183
Db 493 GAACCTGATTTTTTTCGGATGATGATCCTGTCATCACATCTTCTGGAATTCG 552
Qy 184 IleProIleLeuLeuValAlaTyrrPheSerAlaHisIleTyrrTrpSerLeuTrpIlyArg 203
Db 553 ATCCAGATCATCTTATGCTTATTTCAATGATATTTATTTGAGCCTGTGGAAGCGT 612
Qy 204 GlnIlySerSerArgCyLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGGTGCAAGCCATCTGACCTGACTGCT--GTCCTTCAACATC 669
Qy 224 HisGlyHisSerCyArgGlnAspProAspSerArgAlaThrLeuProAlaArgIlyGln 243
Db 670 TGTGACACTCATTCAGAGGATGATCTTCAAGAGATCTCTTTCGACGACAGAA 729
Qy 244 ThrThrAlaSerLeuGlySerAspIlySerArgArgIlySerSerLeuLeuProSerIle 263
Db 720 GTTCCTGCATCTTTCATTCAGAGAGACAGAGAGAGAGAGATGATCTCATGTTTCTCTCA 789
Qy 264 ArgAlaTyrrIlyAsnSerAsnValIleAlaSerIlyMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATGAATAGCAATACATTCCTTCAAAAGGGTCTTCTTCCCAATCATGAT 849
Qy 284 SerLeuAlaLeuGlnArgGlnIlyHisIleGlnLeuPheArgAlaArgIlySerLeuAlaIly 303
Db 850 TCTGTAGCTCTTCAACCAAGGAACATGTGAATCTTGAAGCCAGAGATTAAGCAAG 909
Qy 304 SerLeuAlaIleLeuLeuAlaIleAphaeAlaIleCystrPaIaProTySerLeuThr 323
Db 910 TCACGGCCATCTCTTACGGGTTTTCGTGTTGGGCTCCATATCTCTGTTCACA 969
Qy 324 ValIleTyrrSerPhePheProGluArganLeuThrIleSerThrTrpTyriIsthAla 343
Db 970 ATTGCTTCCTTCAATTTATCTTCACGAAAGGCTCTTAATCAGTTGGTATGAATTGCA 1029
Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValaAnProPheLeuTyProleuCyshiIlyS 363
Db 1030 TTTTGCTTCACGTGTTCAATTCCTTTCGCAATCTCTTTGTATCCATGTGTCAANG 1089
Qy 364 ArgPheGlnIlyAlaPheLeuIlyIleuProValArgArgGlnSerThrPro--Pro 382

Db 1090 CGCTTCAAAAGCGCTTCTGAAATATTTGTATATAAAAGCACCTCTACCATCACAA 1149
QY 383 HIAAANAAGSer11eSerThr 389
Db 1150 CACAGTCGGTCAGTATCTTCT 1170

Search completed: August 5, 2005, 23:02:00
Job time : 724 secs

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OM protein - protein search, using sw model

Run on: August 3, 2005, 01:47:48 ; Search time 40 Seconds
(without alignments)
935.708 Million cell updates/sec

Title: US-10-626-398-10

Perfect score: 2036

Sequence: 1 MLANNSTALTSIKISLFL.....LKILPVRQSTPPHNRISST 389

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1308.5	64.3	390	2 JC7566	histamine H4 recep
2	414	20.3	639	2 A55019	muscarinic acetyl
3	413.5	20.3	590	2 S47572	muscarinic acetyl
4	410	20.1	486	2 JC1415	histamine H1 recep
5	409.5	20.1	589	2 A29476	muscarinic acetyl
6	407.5	20.0	590	2 S01114	muscarinic acetyl
7	406	19.9	488	2 I56507	histamine H1 recep
8	404.5	19.9	589	2 B29514	muscarinic acetyl
9	403.5	19.8	590	2 S10128	muscarinic acetyl
10	402.5	19.8	531	2 JT0531	muscarinic acetyl
11	392	19.3	466	2 I57959	alpha-1C adrenerg
12	390.5	19.2	460	2 I51837	muscarinic recepto
13	390.5	19.2	460	2 A29514	muscarinic acetyl
14	390.5	19.2	532	2 JT0530	muscarinic acetyl
15	389.5	19.1	460	2 S09508	muscarinic acetyl
16	388.5	19.1	460	2 A24325	muscarinic acetyl
17	386.5	19.0	487	2 JC2495	histamine H1 recep
18	385.5	18.9	429	2 S65656	alpha-1C adrenerg
19	385.5	18.9	466	2 JN0765	alpha-1C adrenerg
20	385.5	18.9	499	2 S65657	alpha-1C adrenerg
21	384.5	18.9	466	2 A35375	alpha-1C adrenerg
22	380.5	18.7	491	2 A41632	histamine H1 recep
23	379.5	18.6	490	2 A35546	muscarinic acetyl
24	378	18.6	377	2 A53379	serotonin receptor
25	376.5	18.5	515	2 A40491	alpha-1B adrenerg
26	373.5	18.3	517	2 A45121	alpha-1B adrenerg
27	373	18.3	466	2 S10126	muscarinic acetyl
28	372.5	18.3	460	2 A31897	muscarinic acetyl
29	372	18.3	466	2 A27386	muscarinic acetyl

30	371	18.2	400	2 G00013	D3 dopamine recept
31	371	18.2	466	2 S10856	muscarinic acetyl
32	370	18.2	386	2 S18637	serotonin receptor
33	370	18.2	400	2 G01977	d3 dopamine recept
34	369	18.1	386	2 A42688	serotonin receptor
35	368	18.1	377	2 B30341	G protein-coupled
36	368	18.1	379	2 JC6178	serotonin receptor
37	368	18.1	479	2 S33776	muscarinic acetyl
38	368	18.1	484	2 S58868	G protein-coupled
39	366.5	18.0	515	2 JC1525	alpha-1B adrenerg
40	366	18.0	390	2 JN0268	serotonin receptor
41	365.5	18.0	572	2 I39369	alpha-1A adrenerg
42	364.5	17.9	501	2 JH0447	alpha-1A adrenerg
43	364	17.9	479	2 S10127	muscarinic acetyl
44	363	17.8	466	2 A40972	muscarinic acetyl
45	363	17.8	501	2 T18863	hypothetical prote

ALIGNMENTS

RESULT 1

JC7566 histamine H4 receptor, HH4R - human

C:Species: Homo sapiens (man)

C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C/Accession: JC7566

R:Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.

Biochem. Biophys. Res. Commun. 279, 615-620, 2000

A>Title: Molecular cloning and characterization of a new human histamine receptor, HH4R.

A/Reference number: JC7566; NCID: 20568725; PMID:11118334

A/Contents: Leukocyte

A/Accession: JC7566

A/Molecule type: mRNA

A/Residues: 1-390 <NA>

A/Cross-references: UNIPROT:Q9H3N8; DDBJ:AB045370

A/Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled

A/Genetics:

A/Genes: hh4r

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match	Score	64.3%	Score	1308.5	DB 2	Length	390
Best Local Similarity	65.1%	Pred. No.	1.4e-98				
Matches	252	Conservative	48	Mismatches	84	Indels	3
QY	5	NSTIALT-SIKISLFLMLAIATMGVVTIATIVDRNLRRKNYFFLNATIDFFV	63				
DB	5	NSTINLSLSTRVTLAFMSLVAFATMGVALVTLAFVDKLNRRSSYFFLNATIDFFV	64				
QY	64	GAIAIPLYIPSSLTWTSGKQACVFWLITDYLLCTASVYNYVLSYDRQSVSNVWYRA	123				
DB	65	GAISIPLYIPHTLFWDPGKEICVFWLITDYLLCTASVYNYVLSYDRQSVSNVWYRA	124				
QY	124	CHSGTWKIAOWAVIPEFMTNGPMLISDQNSNTCEBGFLLKWFALPTSLEFL	183				
DB	125	QHTGVAKITLVAAVAVLAFVNGPMLIVSEKSDGSCBEPFSEFWIATISFLFV	184				
QY	184	IPILLVAYSAHVYSLMREKLSRCLSHVLPSSDSSSDHGSCQDPDSRATLPARKS	243				
DB	185	IPVILVAYPNNVNIYSLMREKLSRCLSHVLPSSDSSSDHGSCQDPDSRATLPARKS	243				
QY	244	TTASLGSDSKRRKSLPISIRAYKSNVATSKWGFVSHSDSLAQQREHILPRARKLAK	303				
DB	244	VPSFHSERQRRKSLPISIRAYKSNVATSKWGFVSHSDSLAQQREHILPRARKLAK	303				
QY	304	SLATLAAFAICWAPYSLTIVYSPERNLTGSTVYTAFWLQWNSFVNPFLYPLCHK	363				
DB	304	SLATLGVAVCAWAPYSLTIVYSPERNLTGSTVYTAFWLQWNSFVNPFLYPLCHK	363				
QY	364	RFOKAFKLKLPVRQSTP-PHNRISST 389					
DB	364	RFOKAFKLKLCIKOPLPSOHSRVS 390					

RESULT 2
 A:Accession: A55019
 A:Species: Gallus gallus (chicken)
 C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A55019
 R:Gadbut, A.P.; Galper, J.B.
 J. Biol. Chem. 269, 25823-25829, 1994
 A:Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and
 A:Reference number: A55019; MUID:9501493; PMID:7923287
 A:Accession: A55019
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-639 <GAD>
 A:Cross-references: UNIPROT:P49578; GB:L10617; NID:G530097; PIDN:AAA65961.1; PID:G530098
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 20.3%; Score 414; DB 2; Length 639;
 Best Local Similarity 23.4%; Pred. No. 8.9e-26;
 Matches 125; Conservative 83; Mismatches 145; Indels 182; Gaps 16;

QY 15 ISLTFLMSLLAIALMLGNVAVVLAIVDRNLRHSNYPFLNALADFFVGAIALPLIYPS 74
 DB 117 VLIAFLTGIIALVTIIGILVIVSEKVKQKLTANNVFLSLACADLIIGVISNMLFTTY 176
 QY 75 SLT--WTSGKQACVFWLITDYLCTASVYVIVLISYDRYOSVSNVWYRAQSGTWKAT 133
 DB 177 IIMGMAIGNLACDMLSIDYVSNASVWNLVISPDRYFSTRPLTRAKR--TTKAG 234
 QY 134 QMVAV-WISFMTNGPMILISDSWQ--STTECEPGFLKKWYFALPTSLLEFLIP 185
 DB 225 VMIGLAWISFVLMAPALIF--MQYFVGKRTVPDECFIQLSPILTFGTALAAFYLP 291
 QY 186 ILVAVFSAHIYWSLMK-----RQDPDSR-- 202
 DB 292 VTIMSI---LVRIYKETEKRTKELAGLQASGEAEARFVHOTGSSRSLSYELQROS 347
 QY 203 -----REKLSRCLSHPVLP-----DSSSDH----- 224
 DB 348 TKRSRRRYRCHFWLTKMSWEPNTDQGDQEHSSDSMNNDAAASLNSASDEEDIT 407
 QY 225 -----GHSC-----RQDPDSR-- 241
 DB 408 ETRAIYSIVLKLPGHSAILINSTKLPSSEDLNESADELQSDPTDSQKKPKKIQPKSI 467
 QY 242 -----KETTASIGSDSKSRKSSLLPSIRAYKSNVIAASKMGLSHSD 283
 DB 468 GGSFQKSFSLPIQGSARVATASDGISSVTTSALP--LSFKA--TLAKKFAKTRSQ 524
 QY 284 SLALQQRHEILFRARKLAKSLAIIAFAICWAPYSLTIVYSPFERNLTSTWYHTA 343
 DB 525 ---TKRKMSLIRKKAQAQTISALIFAIITWTYNNIMVAVNTCC--DCPKVWNLG 578
 QY 344 FVLQWNSFVNPEFLPLCHKRFQKAFKLIPV-----RROSTPEPHNR 385
 DB 579 YMLCYINSTVNPVCYALCNKMFRTNFKMLLCQCDKRRKRRKQOYQOROSVIFHNR 633

RESULT 3
 S47572
 muscarinic acetylcholine receptor m3 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S47572
 R:Lee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.
 Biochim. Biophys. Acta 1223, 151-154, 1994
 A:Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 re
 A:Reference number: S47572; MUID:94339178; PMID:8061048
 A:Accession: S47572
 A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-590 <LEE>
 A:Cross-references: UNIPROT:P41984; EMBL:U08286; NID:G520465; PIDN:AAA51866.1; PID:G52046
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 20.3%; Score 413.5; DB 2; Length 590;
 Best Local Similarity 24.3%; Pred. No. 8.9e-26;
 Matches 129; Conservative 80; Mismatches 147; Indels 175; Gaps 17;

QY 15 ISLTFLMSLLAIALMLGNVAVVLAIVDRNLRHSNYPFLNALADFFVGAIALPLIYPS 74
 DB 69 VFIAFLGVLAIVTIIIGILVIVSEKVKQKLTANNVFLSLACADLIIGVISNMLF--- 125
 QY 75 SLTY-----WTSGKQACVFWLITDYLCTASVYVIVLISYDRYOSVSNVWYRAQSGTW 129
 DB 126 -TTYIIMRMALGNLACDMLSIDYVSNASVWNLVISPDRYFSTRPLTRAKR--TT 182
 QY 130 KIATQMAV-WISFMTNGPMILISDSWQSTT---ECEPGFLKKWYFALPTSLLEFLI 184
 DB 183 KRAGVMIGLAWISFVLMAPALIFMQYFVGKRTVPDECFIQLSPILTFGTALAAFYM 242
 QY 185 PILVAVFSAHIYWSLMK-----RQDPDSR-- 202
 DB 243 PVTIWTI---LVRIYKETEKRTKELAGLQASGEAEARFVHOTGSSRSLSYELQRO 298
 QY 203 -----REKLSRCLSHPVLP-----DSSSDH----- 224
 DB 299 SMKRSARKRYRCHFWLTKMSWEPNTDQGDQEHSSDSMNNDAAASLNSASDEEDIG 358
 QY 225 -----GHSC-----RQDPDSR--ATLPARKETALGSDK 252
 DB 359 SETRAIYSIVLKLPGHSAILINSTKLPSSEDLNESADELQSDPTDSQKKPKKIQPKSI 418
 QY 253 SRRKS-SLTP-----SIRAYKSNV-----IASKMGFLSHSDSLAL 287
 DB 419 SFQKSFSLPIQLESAYDTAKSDVNSVGKTATPLSPFKEATLAKFALKTRSQ--I 475
 QY 288 QQRHEILFRARKLAKSLAIIAFAICWAPYSLTIVYSPFERNLTSTWYHTAFLW 347
 DB 476 TKRKMSLIRKKAQAQTISALIFAIITWTYNNIMVAVNTCC--SCIPKTYNIGWYLC 533
 QY 348 WNSFVNPEFLPLCHKRFQKAFKLIPV-----RROSTPEPHNR 385
 DB 534 YINSTVNPVCYALCNKMFRTNFKMLLCQCDKRRKRRKQOYQOROSVIFHNR 584

RESULT 4
 JCI1415
 histamine H1 receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: JCI1415
 R:Fujimoto, K.; Horio, Y.; Sugama, K.; Ito, S.; Liu, Y.Q.; Fukui, H.
 Biochem. Biophys. Res. Commun. 190, 294-301, 1993
 A:Title: Genomic cloning of the rat histamine H1 receptor.
 A:Reference number: JCI1415; MUID:93135784; PMID:7678492
 A:Accession: JCI1415
 A:Molecule type: DNA
 A:Residues: 1-486 <FUJ>
 A:Cross-references: UNIPROT:P31390; DBJ:D12800; NID:G220770; PIDN:BA02245.1; PID:G22077
 C:Comment: This Ca2+-mobilizing receptor mediates immune hypersensitivity in peripheral t
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:30-49/Domain: transmembrane #status predicted <TM1>
 F:64-83/Domain: transmembrane #status predicted <TM2>
 F:102-121/Domain: transmembrane #status predicted <TM3>
 F:146-165/Domain: transmembrane #status predicted <TM4>
 F:190-209/Domain: transmembrane #status predicted <TM5>
 F:418-437/Domain: transmembrane #status predicted <TM6>
 F:450-469/Domain: transmembrane #status predicted <TM7>

Query Match 20.1%; Score 410; DB 2; Length 486;
 Best Local Similarity 24.5%; Pred. No. 1.4e-25;

Matches 118; Conservative 85; Mismatches 163; Indels 116; Gaps 14;

QY 1 MLANNSTALTSIKSLTFLMSLAIAMGNVVVLAIFYDRNLRRHSNYFPLNLAAD 60
Db 14 MCEGNRTTAMSPOLLPLVVVLISSILTVGLNLVLVAHSEKRLHTGNYLIVSLSVAD 73
QY 61 FFVGAIAIP---LVIPSSLTWTSKQACVFWLITDYLCTASVYVNLVLSYDRYQSVSN 117
Db 74 LIVAVVAMPKNILVL--IMTKWSLGRPLCLFELMSLMDYASTASIFSVFLCIDRYSVQ 131
QY 118 AVWYRAQSGTGMKATQWAVVAFSFMNGEMILISDSQW-----STTECEPGFLK 169
Db 132 PLRLRLRRTKRAAT--ILGAMFSEFLMVLITL-----GMHFMPPARELBDKCTDPYN 186
QY 170 KMVFLPTSLLEPLIPILVAVFSAHYWSLMKREKLSRCLSHVLPDSG---SSDHG 225
Db 187 VTMFKIMTAIINFPLTLMFLFYKVIYKAV--RRHCGRQLTNGSLPSFSLKLRSDPTK 245
QY 226 HSCR-----QDP-----DSRATLP-----ARKETASLGS DKS 253
Db 246 EGAKKPGRESFPGVLRKPSRDPVGLDQKSTSEDPKMTSPVFSQEGRETRPCFRLLIM 305
QY 254 RRKSLSLPSIPAYKNSNVIAS-----KMGFLSHSDSLALQ-----289
Db 306 QKQSVAGSDVAGSKANDQALSQPKMDEQSLNCTCRISSETSDDQLVLDQQSRTTSDTS 365
QY 290 -----REH-----IELFRARKLASLAILAAFAI 314
Db 366 IEPGPKYKNSGSGNSGLDIKITMKRLRHSRQVSGSLHNRKRKAQKQGFIMAAFIL 425
QY 315 CWAPYSLTTVYISFPPERNLTGSTWYHTAFPLQWPNFNPFLPLCHKRQKQKFLILP 374
Db 426 CWIPYFIFFWVIAC--KSCCEBPMHFTIMLGYNSTLNLPLIYPLCNENPKKTFKKILH 483
QY 375 VR 376
Db 484 IR 485

RESULT 5
A29476
muscarinic acetylcholine receptor M4 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Dec-1988 #text_change 09-Jul-2004
C/Accession: A29476
R/Biran, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 149, 125-132, 1987
A/Title: A novel subtype of muscarinic receptor identified by homology screening.
A/Reference number: A29476; MUID:88077068; PMID:3120722
A/Accession: A29476
A/Molecule type: mRNA
A/Residues: 1-589 <BRA>
A/Cross-references: UNIPROT:P08483; GB:M18088; NID:g202657; PIDN:AAA40659.1; PID:g202655
A/Experimental source: Brain
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane
F/67-90/Domain: transmembrane #status predicted <TM>
F/104-134/Domain: transmembrane #status predicted <TM2>
F/142-163/Domain: transmembrane #status predicted <TM3>
F/184-206/Domain: transmembrane #status predicted <TM4>
F/230-251/Domain: transmembrane #status predicted <TM5>
F/492-512/Domain: transmembrane #status predicted <TM6>
F/527-545/Domain: transmembrane #status predicted <TM7>

Query Match 20.1%; Score 409.5; DB 2; Length 589;
Beet Local Similarity 24.6%; Pred. No. 1.9e-25;
Matches 131; Conservative 81; Mismatches 143; Indels 177; Gaps 17;

QY 15 ISLTFMLAIAMIGNVVLAIFYDRNLRRHSNYFPLNLAADFFVGAIAIPLYPS 74
Db 68 VFIAFLTFGLLVITIGILVITVAFKVKQKLTANNYTLACLADLLIGVISMFL---124
QY 75 SLTY-----WTSKQACVFWLITDYLCTASVYVNLVLSYDRYQSVSNVAVYRAQSGTW 129

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Db      125  -TTTIANRMLAGNLACDMLSLDIDYASNA5VNNLVISDRKFSITRPLITYAKR--TT 181
Qy      130  KIATQVAV-WIFSEPTNGPMILISDSWQNST---ECBPGELKMYFALPTSLLEFLI 184
Db      182  KRAGMIGLAWIYSFLVMAFALIFWQYFVGKRTVPBGEICIGLSEPTTIFGATAIAFYM 241
Qy      185  PILVAVYSAHITYSLWLMKR-EKLSRCLS-----HPVLPSDSSS----- 222
Db      242  PVTIMTI---LYMRIYKTEKRTYKELAGLOASGTEAEAEENFVHPGSSSCSSGYELOOQ 297
Qy      223  -----DHGHSR---QDPSPRATLPARKETAS--- 247
Db      298  GVKRSSRRKYRGCHFVFTTKSWKPSAEOQMDQHSSSDSMNNNNDAAASL---ENSASSDE 353
Qy      248  --LGSD-----KSRKSSLLPSIRAYKSNVYASK----- 275
Db      354  EDIGSETRAIYISVLKLPQHSSILNSTKLPPSSNLOVSNEDLGTVDERAHKLOAQKSM 413
Qy      276  -----MGFLSHSDSLA----- 286
Db      414  GDGDNOCQKDFTKLPQLBSAVDPTGKTSDDTNSADTKTATLPISFKEATLAKRFALKTRSQ 473
Qy      287  LQQRHIEIFRARKLAKSLAILLAAFAICWAPPSLTTVIYSPFBRRLTSGTWHTHFWL 346
Db      474  ITRKRMSLIIKEXKAQOTSAIILLAPFIITMTPINIVLWTF--RDSICPKTYWNLGYWL 531
Qy      347  QMFNSFVNPVLPCLCHKRFQKAFUKILPV-----RROSTPPHNR 385
Db      532  CYNSTVNPVCALCNKTRFTFKMLLLQCQDCKRRKRKOQYOROSVYIFHKR 583

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RESULT 6
S01114
muscarinic acetylcholine receptor M2, glandular - pig
N/Alternate names: muscarinic acetylcholine receptor III
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #ext_change 09-Jul-2004
C/Accession: S01114
R/Rkiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.
FEBS Lett. 235, 257-261, 1988
A/Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonist
A/Reference number: S01114; MUID:88296835; PMID:3402600
A/Accession: S01114
A/Molecule type: DNA
A/Residues: 1-590 <AX1>
A/Cross-references: UNIPROT:P1483; EMBL:X12712; NID:g1861; PIDD:CAA31215.1; PIDD:g1862
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmem
F:68-91/Domain: transmembrane #status predicted <TM1>
F:105-125/Domain: transmembrane #status predicted <TM2>
F:143-164/Domain: transmembrane #status predicted <TM3>
F:185-207/Domain: transmembrane #status predicted <TM4>
F:231-255/Domain: transmembrane #status predicted <TM5>
F:493-513/Domain: transmembrane #status predicted <TM6>
F:528-546/Domain: transmembrane #status predicted <TM7>

Query Match      20.0%; Score 407.5; DB 2; Length 590;
Best Local Similarity 24.1%; Pred. No. 2, Re-25;
Matches 129; Conservative 83; Mismatches 140; Indels 183; Gaps 17;

OY 15 ISLTFLMSLTAIAMLGNVNVILAFVDRNLHRSNVPFLNLAIADFFVGAIAPLYIPS 74
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 69 VFIALTLGLTALVTIIIGNLTIVAFKVNQKLTNNVYFLSLACADIIIGVISNNLP--- 125
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

OY 75 SITV-----WTSKQACVFWLITDYLLCTASVYNIVLISDYQVSNNAVYRAQHSQIW 129
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 126 -TTYIINRMWALGNLACDMLSLIDVYASNASVNNLLIVISDRYFSTIRPLTYRAKR--TT 182
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

OY 130 KIATQMVAV-WIEFMTNGEMLLISDSQNSNT---ECSPGGLKKVYFALPLPSLAEFLI 184
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 183 KRAVGWIGLAWISFLWAPALLFWQYFVGKRVPPGECFTQFLSEPTTTFGTALAAFYM 242
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

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QY 15 ISLTPLMSLAIAIMGNVVVILAFIVDRNLRRHSNFFPLNLAIADPFVGAIAPIPIYPS 74
 Db 68 VFIAFLTGFLATLTIIGNIIVIAFKVNNKQTKVNNYFLLSLACADLIIGVISMNLF--- 124
 QY 75 SLTY-----WTSKQACVFWLITDYLLCTASVYNIIVLISDRYQSVSNVAVRAQSGTW 129
 Db 125 -TTYIIMNRWALCNLACDLWLSIDYVANSVNNLWLVISPDYFSITRPLTYBAKRT--TK 182
 QY 130 KIATQVAVVIFSPMTNGPMILISDSQNST-----ECEPGFLKKWYFALPTSLLEFLIP 185
 Db 183 RGVWIGLAWVISFVLMAPAILFWQYFVGKRTVPBGECIPIQFLEPTITFGTIAIAFYMP 242
 QY 186 ILVAVFSAHIYWSLWK- EKLSRCL-----HPVLPSDSSS----- 222
 Db 243 VITMTI-----LVYRIYKEPEKRTKELAGLQASGTEAEAFVHPGSSRSCSSYELQQG 298
 QY 223 -----DHGSCR---QDPDSRATLPARKETAS--- 247
 Db 299 VKRSRRKYGRCHFMTTKSWKPSAEQMDQDHSSSDSMNNNDAAATL---ENSASDEE 354
 QY 248 -IGSD-----KRRKSLPSTRAYKNSVIAK----- 275
 Db 355 DIGSETRAIYSIVLKLPGHSSILNSTKLPSSDNLQVSNEDLGTVDVERNAHKLQAKSMG 414
 QY 276 -----MGFLSHSDSLA-----L 287
 Db 415 DGNCKQDPTKLPQLQESAVDTGKTSPTNSSADKTTATLPLSFKEATLAKRFLKTRSQI 474
 QY 288 QOREHIELFRARKLAKSLAILAFAICWAPYSLTTVIYSFPPERNLTKSTWYHTAFWLG 347
 Db 475 TKRKMSLTKKKAQTLAISAILAFIITWTPYNIWLVNTFCD--SCIPKYWNLGWYLC 532
 QY 348 WFSFNPPLFLYPLCHKRFOKAFILKLPV-----RROSTPPHNR 385
 Db 533 YINSTVNPVCYALCNKTFRTFTLLCCQCKRRKROQYQOROSVIFHKR 583

RESULT 9

S10128
 muscarinic acetylcholine receptor M4 - human
 C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
 C/Accession: S10128
 R.Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramechandran, J.; Capon, D.J.
 EMBO J. 6, 3923-3929, 1987
 A/Title: Distinct primary structures, ligand-binding properties and tissue-specific exp
 A/Reference number: S04326; WUID:8816632; PMID:3443095
 A/Accession: S10128
 A/Molecule type: DNA
 A/Residues: 1-590 <PER>
 A/Cross-references: UNIPROT:P20309; EMBL:X15266; NID:932323; PDB:1CMA3337.1; PID:932324
 C/Superfamily: Vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
 F:68-95/Domain: transmembrane #status predicted <TM1>
 F:105-131/Domain: transmembrane #status predicted <TM2>
 F:143-164/Domain: transmembrane #status predicted <TM3>
 F:185-207/Domain: transmembrane #status predicted <TM4>
 F:231-252/Domain: transmembrane #status predicted <TM5>
 F:493-513/Domain: transmembrane #status predicted <TM6>
 F:525-546/Domain: transmembrane #status predicted <TM7>
 F:5,6,15,41/Binding site: carbohydrate (Asn) #status predicted

Query Match 19.8%; Score 403.5; DB 2; Length 590;

Best Local Similarity 23.1%; Pred. No. 5.8e-25;

Matches 124; Conservative 83; Mismatches 146; Indels 183; Gaps 16;

QY 15 ISLTPLMSLAIAIMGNVVVILAFIVDRNLRRHSNFFPLNLAIADPFVGAIAPIPIYPS 74
 Db 68 VFIAFLTGFLATLTIIGNIIVIAFKVNNKQTKVNNYFLLSLACADLIIGVISMNLF--- 125
 QY 75 SLTY-----WTSKQACVFWLITDYLLCTASVYNIIVLISDRYQSVSNVAVRAQSGTW 129
 Db 125 -TTYIIMNRWALCNLACDLWLVISPDYFSITRPLTYBAKRT--TT 182

QY 130 KIATQVAVVIFSPMTNGPMILISDSQNST-----ECEPGFLKKWYFALPTSLLEFLIP 184
 Db 183 RGVWIGLAWVISFVLMAPAILFWQYFVGKRTVPBGECIPIQFLEPTITFGTIAIAFYM 242
 QY 185 ILVAVFSAHIYWSLWK- EKLSRCL-----HPVLPSDSSS----- 202
 Db 243 VITMTI-----LVYRIYKEPEKRTKELAGLQASGTEAEAFVHPGSSRSCSSYELQQG 298
 QY 203 -----REKLSRC-----LSHPVLPSDSSSDH----- 224
 Db 299 SMKRSNRKYGRCCHFMTTKSWKPSAEQMDQDHSSSDSMNNNDAAASLENSASDEEDIG 358
 QY 225 -----GHSC-----ROD----- 231
 Db 359 SETRAIYSIVLKLPGHSSILNSTKLPSSDNLQVPEBELGVDERKADKLQAKSYDDG 418
 QY 232 --PDSRATLPARKET-----TASIGSDKSRKSLPSTRAYKNSVIAKMGFLSHSD 283
 Db 419 SPKSPSKLPQLQESAVDTGKTSPTNSSADKTTATLPLSFKEATLAKRFLKTRSQI 474
 QY 284 SLAQOREHIELFRARKLAKSLAILAFAICWAPYSLTTVIYSFPPERNLTKSTWYHTA 343
 Db 475 ---ITRKMSLTKKKAQTLAISAILAFIITWTPYNIWLVNTFCD--SCIPKTFWNLG 529
 QY 344 FWLQWNSFVNPPLFLYPLCHKRFOKAFILKLPV-----RROSTPPHNR 386
 Db 530 YWLCYINSTVNPVCYALCNKTFRTFTLLCCQCKRRKROQYQOROSVIFHKRA 585

RESULT 10

JT0531
 muscarinic acetylcholine receptor M5 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C/Accession: JT0531; A33354; C37121
 R.Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.
 Neuron 1, 403-410, 1988
 A/Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor
 A/Reference number: JT0530; WUID:9016521; PMID:3272174
 A/Accession: JT0531
 A/Molecule type: DNA
 A/Residues: 1-531 <BON>
 A/Cross-references: UNIPROT:P08911
 R.Liao, C.F.; Thiemmen, A.P.N.; Joho, R.; Barberis, C.; Birnbaumer, M.; Birnbaumer, L.
 J. Biol. Chem. 264, 7328-7337, 1989
 A/Title: Molecular cloning and expression of a fifth muscarinic acetylcholine receptor.
 A/Reference number: A33354; WUID:89214170; PMID:2540186
 A/Accession: A33354
 A/Molecule type: DNA
 A/Residues: 1-531 <LHA>
 A/Cross-references: GB:W2925; NID:920531; PDB:AAA4157.1; PID:9205312; GB:J04706
 C/Superfamily: Vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
 F:29-52/Domain: transmembrane #status predicted <TM1>
 F:66-86/Domain: transmembrane #status predicted <TM2>
 F:104-125/Domain: transmembrane #status predicted <TM3>
 F:146-168/Domain: transmembrane #status predicted <TM4>
 F:191-213/Domain: transmembrane #status predicted <TM5>
 F:443-463/Domain: transmembrane #status predicted <TM6>
 F:478-496/Domain: transmembrane #status predicted <TM7>
 F:7,12/Binding site: carbohydrate (Asn) (covalent) #status predicted


```

Db      94 GTLACDLMALDQVNASVSNVNLISFDHYFSVTRPLSYRAKR--TPRRALMIGLAWL 151
Qy      141 FEFMTNGPMILISDSQWNTTE-----CEGFLLKKMYPALPTSLLEPIPLILVAYRS 193
Db      152 VSEFVLMAPAILF---WQYLVGERTVLACQCYIOFLQPIITFTGTAMAAFLPVTVA---- 204
Qy      194 AHYMSLMREKLSRCLSHVLP-----SDSSSDH-----GHSGR-- 229
Db      205 CTLVWRIT-RETENRARELALAQSETPGKGGSSSSSSSSSSSGPARGSPSPGRCRC 263
Qy      230 -----QDPDSRATLPARKETATASIGSDKSRKSS 259
Db      264 RAPRLAQVSWKEEEDSGMESLTSSEGEERGSEVVKMPVDSBAQAPTKQPPKSSP 323
Qy      260 LPSIRAYKSNVYASIKMGFLSHSDSLAQOREHIELFPAKRLAKSLAILLAFAICWAP 319
Db      324 NTVKRPETKKGRDGGGOKPRGKEOLA--KRKTFSLVKEKKARTLSAILLAFLITWTPY 381
Qy      320 SLTTVYISFFPERNLTKSTWYHTAPFLQWPNFVNFLPLCHKRPQKAFKILPVR 376
Db      382 NIMVLVSTFC--KDCVPEITLMEIGWMLCYVNSTVNPWCALCNKARDFTRILLCR 436

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RESULT 13

A29514

muscarinic acetylcholine receptor M1 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C/Accession: A94518; A94293; A37121; A29514

R/Bonner, T.I.

Submitted to GenBank, July 1987

A/Reference number: A94518

A/Accession: A94518

A/Molecule type: mRNA

A/Residues: 1-460 <BO1>

A/Cross-references: UNIPROT:P08482

R/Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R. Science 237, 527-532, 1987

A/Title: Identification of a family of muscarinic acetylcholine receptor genes.

A/Reference number: A94293; PMID:87263421; PMID:3037705

A/Accession: A94293

A/Molecule type: mRNA

A/Residues: 1-227;338-460 <BO2>

A/Experimental source: cerebellar cortex

A/Note: only a part of the protein translation is given, none of the nucleotide sequence

R/Kurenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C. J. Biol. Chem. 265, 13702-13708, 1990

A/Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invc

A/Reference number: A37121; PMID:90337982; PMID:2380182

A/Accession: A37121

A/Status: preliminary

A/Molecule type: protein

A/Residues: 62-124 <KUR>

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho

F/25-50/Domain: transmembrane #status predicted <TM1>

F/62-93/Domain: transmembrane #status predicted <TM2>

F/100-121/Domain: transmembrane #status predicted <TM3>

F/142-168/Domain: transmembrane #status predicted <TM4>

F/187-209/Domain: transmembrane #status predicted <TM5>

F/167-387/Domain: transmembrane #status predicted <TM6>

F/402-420/Domain: transmembrane #status predicted <TM7>

F/2,12/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.2%; Score 390.5; DB 2; Length 460;

Best Local Similarity 27.3%; Pred. No. 4.9e-24;

Matches 114; Conservative 68; Mismatches 158; Indels 77; Gaps 12;

Qy 23 LLAIALMGVNVVILAFYDNRILRHSNFFFLALADFFVGAIAPLYPSSLT-YWTS 81

Db 34 LLSLATVGTNLVLIISFKVTTELKTVNFFLLSLACADLLIGTGSNMLYTLTMGMWAL 93

```

Qy      82 GKQACVFWLITDYLCTASVNVILISYDRYOSVNAWYRAQSGTWKATQWAV-WI 140
Db      94 GTLACDLMALDQVNASVSNVNLISFDHYFSVTRPLSYRAKR--TPRRALMIGLAWL 151
Qy      141 FEFMTNGPMILISDSQWNTTE-----CEGFLLKKMYPALPTSLLEPIPLILVAYRS 193
Db      152 VSEFVLMAPAILF---WQYLVGERTVLACQCYIOFLQPIITFTGTAMAAFLPVTVA---- 204
Qy      194 AHYMSLMREKLSRCLSHVLP-----SDSSSDH-----GHSGR-- 229
Db      205 CTLVWRIT-RETENRARELALAQSETPGKGGSSSSSSSSSGPARGSPSPGRCRC 263
Qy      230 -----QDPDSRATLPARKETATASIGSDKSRKSS 259
Db      264 RAPRLAQVSWKEEEDSGMESLTSSEGEERGSEVVKMPVDSBAQAPTKQPPKSSP 323
Qy      260 LPSIRAYKSNVYASIKMGFLSHSDSLAQOREHIELFPAKRLAKSLAILLAFAICWAP 319
Db      324 NTVKRPETKKGRDGGGOKPRGKEOLA--KRKTFSLVKEKKARTLSAILLAFLITWTPY 381
Qy      320 SLTTVYISFFPERNLTKSTWYHTAPFLQWPNFVNFLPLCHKRPQKAFKILPVR 376
Db      382 NIMVLVSTFC--KDCVPEITLMEIGWMLCYVNSTVNPWCALCNKARDFTRILLCR 436

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RESULT 14

JT0530

muscarinic acetylcholine receptor M5 - human

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000

C/Accession: JT0530

R/Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J. Neuron 1, 403-410, 1988

A/Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor

A/Reference number: JT0530; PMID:90166521; PMID:3272174

A/Accession: JT0530

A/Molecule type: DNA

A/Residues: 1-532 <BON>

C/Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neurocr

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho

F/30-53/Domain: transmembrane #status predicted <TM1>

F/67-87/Domain: transmembrane #status predicted <TM2>

F/105-126/Domain: transmembrane #status predicted <TM3>

F/147-169/Domain: transmembrane #status predicted <TM4>

F/192-214/Domain: transmembrane #status predicted <TM5>

F/444-464/Domain: transmembrane #status predicted <TM6>

F/479-498/Domain: transmembrane #status predicted <TM7>

F/8,13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.2%; Score 390.5; DB 2; Length 532;

Best Local Similarity 24.2%; Pred. No. 5.8e-24;

Matches 121; Conservative 78; Mismatches 146; Indels 155; Gaps 16;

Qy 15 ISLTFMISLLAIAIMGVNVVILAFYDNRILRHSNFFFLALADFFVGAIAPLYIPS 74

Db 31 ITIAAVTAVSLITVIGNVLVMSFVNSQLKTVNFFLLSLACADLLIGISIRPMNLV--- 87

Qy 75 SLTY-----WTSGKQACVFWLITDYLCTASVNVILISYDRYOSVNAWYRAQSGTW 129

Db 88 -TTYILMGWALGSLACDLMALDQVNASVSNVNLISFDHYFSVTRPLSYRAKR--TP 144

Qy 130 KIATQWAV-WIFSFTNGPMILISDSQWNTTE-----STTECEGFLKKMYPALPTSL 181

Db 145 KRGIMIGLAWLISFLMAPAIL---CWQYLVGKRTVPLDECOIQLSEPTITFGAIAA 201

Qy 182 FLIPLILVYFAHYT-----W-KREKLSRCLSHVLPDSSSSDHGS 197

Db 202 FYIPVSVMTILYCRITREBKRKDLADIQSDSVTKAKRPAHAAALRSCLRCRPTL 261

Qy 198 -----WSL-----W-KREKLSRCLSHVLPDSSSSDHGS 227

Db 262 AQERHQASWSSSRSTSTGKPSQATGPSANWAKAEQLTTCSSYP-----SSDEDKP 315

QY 228 C-----KODPSRATLPARKETTASLGSDKS--RRKSLPSIRAY--KNSN 270
 DB 316 ATDPVLQVYVYKSGKESPEEFESABETETFPVKAETKESDVTPTVLLSPAANRPKQX 375
 QY 271 VIASQMGFLSHSD-----SLAQOREHIELF 296
 DB 376 CVAAYKFRVLVVKADGQOETNNGCHKVKIMPCPPVAKPEPTKGLNPNPSHQTKRKRVVLV 435
 QY 297 RARKLAKSLAIIILAAFAICWAPYSLTIVYSFPERNLKSTWHTAFMLQMFNSPVNPF 356
 DB 436 KERKAQUTISAILLFIITWTPIYNI-MVLVSTFCDCVCFVTLN-HLGWLCYVNSTVNI 493
 QY 357 LYPICHRKRFQKAFELKILPVR 376
 DB 494 CVALCNRTFRKTKFKMLLCLR 513

RESULT 15

S09508
 muscarinic acetylcholine receptor M1 - human

C.Species: Homo sapiens (man)

C.Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 03-Jul-2004

C.Accession: S09508; S06327; S04326

R.Chapman, C.G.; Browne, M.J.

Nucleic Acids Res. 18, 2191, 1990

A.Title: Isolation of the human m1 (Hm1) muscarinic acetylcholine receptor gene by PCR a

A.Reference number: S09508; MUID:90245684; PMID:5336407

A.Accession: S09508
 A>Status: nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA

A.Residues: 1-460 <CHA>

A.Cross-references: UNIPROT:P11229; EMBL:X52068; NID:G34450; PIDN:CAA36291.1; PID:G34451

A.Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990

R.Allard, W.J.; Sigal, I.S.; Dixon, R.A.F.

Nucleic Acids Res. 15, 10604, 1987

A.Title: Sequence of the gene encoding the human M1 muscarinic acetylcholine receptor.

A.Reference number: S06327; MUID:88096607; PMID:3697105

A.Accession: S06327

A.Molecule type: DNA

A.Residues: 1-460 <ALL>

A.Cross-references: GB:Y00508; GB:M5128; NID:G297405; PIDN:CAA68560.1; PID:G297406

R.Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.

EMBO J. 6, 3923-3929, 1987

A.Title: Distinct primary structures, ligand-binding properties and tissue-specific expr

A.Reference number: S04326; MUID:88166632; PMID:3443095

A.Accession: S04326

A.Molecule type: DNA

A.Residues: 1-172, 'M', 174-460 <PER>

A.Cross-references: EMBL:X15263; NID:G32317; PIDN:CAA33334.1; PID:G32318

C.Superfamily: Vertebrate rhodopsin

C.Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho

F.25-50/Domain: transmembrane #status predicted <TM1>

F.62-93/Domain: transmembrane #status predicted <TM2>

F.100-121/Domain: transmembrane #status predicted <TM3>

F.142-168/Domain: transmembrane #status predicted <TM4>

F.187-209/Domain: transmembrane #status predicted <TM5>

F.367-387/Domain: transmembrane #status predicted <TM6>

F.402-420/Domain: transmembrane #status predicted <TM7>

F.2,12/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 19.1%; Score 389.5; DB 2; length 460;

Best Local Similarity 27.1%; Pred. No. 5, 9e-24;

Matches 115; Conservative 72; Mismatches 145; Indels 93; Gaps 15;

QY 23 LLAIIIMGNVVVYIAFYDRNLRRHSNFFFLNLAIDFFGAIAPLYIPSSLT-YWTS 81

DB 34 LLSLATVIGNLVLISFKVNTLKTNNFLLSLACADLIIGTFSMNLTYTILMGHWAL 93

QY 82 GKQACVFMILITDYLCSTASVNIIVLISYRQSVSNAAVYRAOHSQGTWIAQWAV-WI 140

DB 94 GTLACDMLALDLYVSNASVNWMLLISFDRYPSVTRPLSYRAKR--TPRRALMIGLAWL 151

QY 141 FSPMTNGFMILISDSWONSTTE-----CEBGLKKWYFALPTSLLEFLIPILLVAYFS 193
 DB 152 VSFVLMAPIILF---WQVLGERTVLAGQCYIQFLSQPIITFGTMAAFYLPVTW---- 204
 QY 194 AHYWSLMKREKLRCLSHPVLP-----SDSSSDH-----GHSR-- 229
 DB 205 CTLYWRIY-RETTENRARELALQGETPGKGGSSSSSERSGPGAEGSPETPPGRCCRC 263
 QY 230 -----ODPSRATLPARKETTASLGSDKSRRKSLPSI----- 263
 DB 264 RAPLLQAYSKKEEEDSGMESL-----TSSEGEPSGVIVIKMPVDEAQAPTKQ 317
 QY 264 --RAYKSNVIASQMGFLSHSDSLA-----LQOREHIELFRARLAKSLAIIILAA 311
 DB 318 PPRSSPMTVKRPTKKG---RDRAGKQKPRGKEQLAKRTFSLYKKAARTLSAIIILA 373
 QY 312 FAICWAPYSLTIVYSFPERNLKSTWHTAFMLQMFNSPVNPFYPLCHRFQKAPLK 371
 DB 374 FILTWTPIYNIWLVSTFC--KDCVPEIIMELGYMLCYVNSTINPCVYALCNKAFRDTFRL 431
 QY 372 ILPVR 376
 DB 432 LILCR 436

Search completed: August 3, 2005, 01:57:48
 Job time : 43 secs

GenCore version 5.1.6
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OW protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2005, 20:15:21 ; Search time 3171 Seconds
(without alignments)
4669.505 Million cell updates/sec

Title: US-10-626-398-10
Perfect score: 2036
Sequence: 1 MLANNSTALTSIKISLFTL.....LKILPVROSTPPHNSIST 389

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame_p2n.model -DEV=rlp
-Q=cgnt_1/USPTO.spool_p/US10626398/runat_02082005.155808.2927/app_query.fasta.1.583
-DB=EST -QPMT=fastap -SUFFIX=ext -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pro -NORP=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10626398.ccgcn_1.1.5180@runat_02082005.155808.2927 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_ges1.*
9: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	817	40.1	839	5	BX643713 DKFZp781C
2	806.5	39.6	704	7	CF147821 AGENCOURT
3	460	22.6	732	7	CF147822 AGENCOURT
4	443.5	21.8	721	7	CO959034 AGENCOURT
5	404.5	19.9	1770	3	AY400784 Mus muscu
6	404.5	19.9	3171	3	AK080950 Mus muscu
7	403.5	19.8	1773	9	AY400782 Homo sapi
8	402	19.7	2760	3	AK032763 Mus muscu
9	402	19.7	2831	3	AK047070 Mus muscu

10	402	19.7	2979	3	AK038480	AK038480 Mus muscu
11	402	19.7	3783	3	AK046607	AK046607 Mus muscu
12	394.5	19.4	853	6	CD326085	CD326085 AGENCOURT
13	391.5	19.2	672	6	CB556920	CB556920 AKMNNIC:U
14	391	19.2	1401	9	AY399428	AY399428 Mus muscu
15	391	19.2	4124	3	AK085653	AK085653 Mus muscu
16	388.5	19.1	4135	3	AK079597	AK079597 Mus muscu
17	388.5	19.1	3816	3	AK081248	AK081248 Mus muscu
18	384	18.9	1401	9	AY399426	AY399426 Homo sapi
19	378	18.6	1124	9	AY418218	AY418218 Homo sapi
20	376.5	18.5	1764	3	BC018330	BC018330 Mus muscu
21	376.5	18.5	2611	3	AK004891	AK004891 Mus muscu
22	376.5	18.5	3050	3	AK038777	AK038777 Mus muscu
23	370	18.2	1203	9	AY407499	AY407499 Homo sapi
24	369	18.1	1161	9	AY415607	AY415607 Mus muscu
25	368	18.1	1203	9	AY407500	AY407500 Pan trogl
26	368	18.1	1440	9	AY404936	AY404936 Mus muscu
27	366	18.0	1173	9	AY415605	AY415605 Homo sapi
28	366	18.0	1440	9	AY404935	AY404935 Pan trogl
29	364	17.9	1440	9	AY404934	AY404934 Homo sapi
30	361	17.7	1125	9	AY418220	AY418220 Mus muscu
31	361	17.7	1173	9	AY415606	AY415606 Pan trogl
32	361	17.7	2908	3	AK082016	AK082016 Mus muscu
33	356.5	17.5	1200	9	AY407501	AY407501 Mus muscu
34	356	17.5	2232	3	CR606112	CR606112 full-length
35	352.5	17.3	1072	9	AY398880	AY398880 Homo sapi
36	348	17.1	1332	9	AY418851	AY418851 Homo sapi
37	347	17.0	1347	9	AY416858	AY416858 Mus muscu
38	347	17.0	2578	3	AK045364	AK045364 Mus muscu
39	345.5	17.0	1072	9	AY398881	AY398881 Pan trogl
40	342.5	16.8	1335	9	AY418853	AY418853 Mus muscu
41	336.5	16.5	716	7	CN423054	CN423054 170004245
42	335.5	16.5	1069	9	AY398882	AY398882 Mus muscu
43	328.5	16.1	499	2	BF567556	BF567556 UT-R-B00
44	328	16.1	1167	9	AY416975	AY416975 Mus muscu
45	327	16.1	1141	9	AY416974	AY416974 Pan trogl

ALIGNMENTS

RESULT 1
BX643713 839 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp781C0629.F1.781 (synonym: hlc4) Homo sapiens cDNA clone
LOCUS BX643713
ACCESSION DKFZp781C0629.5, mRNA sequence.
VERSION BX643713.1 GI:34478046
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 839)
AUTHORS Lauber, D., Bahr, A., Mewes, H.W., Weill, B., Amlid, C., Osanger, A.,
Rodo, G., Han, M., and Wiemann, S.
TITLE EST (Lauber, J., Bahr, A., Mewes, H.W., Weill, B., Amlid, C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS

FEATURES

FEATURES
source
1. 839
/organism="Homo sapiens"
/mol_type="mRNA"

MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the CDNA sequencing
consortium of the German Genome Project.
No 5' sequence available.
This clone (DKFZp781C0629) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 839
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="DKFZP781C0629"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="781 (synonym: hlc64)"
/note="Vector: pSPORT1_Sfi; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Alignment Scores:

Pred. No.: 1,846-73 Length: 839
Score: 817.00 Matches: 160
Percent Similarity: 78.69% Conservative: 32
Best Local Similarity: 65.57% Mismatches: 50
Query Match: 40.13% Indels: 3
DB: 5 Gaps: 2

US-10-626-398-10 (1-389) x BK643713 (1-839)

5 AanserThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
108 AATAGACAAATCAATTTATTCACAGACACTCGTGTACTTTCAGATTTTATGTCCTTA 167
24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
168 GTAGCTTTTGTCTAATATGCTAGAAATGCTTGTCTATTGCTTTGCTGGACAAA 227
44 AenLeuArgHisArgSerAsnTyrrPheLeuAsnLeuAlaIleAlaAspPheVal 63
228 AACCTTAGACATCGAAGTAGTATTTTCTTAACTTGCCCACTCTGACTCTTTG 287
64 G1yAlaIleAlaIleProLeuTyrrIleProSerSerLeuThrTyrrPheSerGlyLys 83
288 GGTGGATCTTCATCTCTTGTATACATCCCTCACACAGCTTTGGAATGGATTGGAAAG 347
84 G1nAlaCysValPheTrpLeuIleThrAspTyrrLeuLeuCysThrAlaSerValTyra 103
348 GAAACTGTGTATTTTGGCTCACTACTGACTGACTGCTGTATGTATGACACATCTGATATAAC 407
104 ILeValIleIleSerTyrrAspArgTyrrGlnSerValSerAsnAlaValTyrrTyrrAla 123
408 ATTGCTCTATCATGCTATATGATGATCTGCTGACGTCTCAAAAGCTGTGTCTTATGAACT 467
124 G1nHisSerGlyThrTrpValIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
468 CAACATACGTGGGTCTTGAAGATTGTTACTCGATGCTGGCGTTGGTGGCGGCTTC 527
144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGlyCys 163
528 TTAGTGAATGGGCAATGATTTCTAGTTTCAGAGTCTTGAAGAGATGAAGTGTGATGT 587
164 G1uProGlyPheLeuLysLysTrpTyrrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
588 GAACCTGGAATTTTTCGGAATGATGATCCTTGGCATCATCATCTTCTTGGAAATTCGG 647
184 ILeProIleLeuLeuValAlaTyrrPheSerAlaHisIleTyrrPheSerLeuTrpLysArg 203
648 ATCCCGCATCTAGTCTTATGCTTATTTCAACATGAATATTATTTAGAGCGCTGGAAAGCGT 707
204 G1uLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
708 GATCATCTAGTAGAGGCAAGCCATCTGAGCTGACTGCTGTCTCTTCCACATCTGT- 766
224 H1sGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaTrgylsGlu 243
767 ---GGACATCTCATTCAGAGTAGACTATCTTCAAGAGATCTCTTTTCGATCGACAGAA 823
244 ThrThrAlaSer 247
824 GTTCCCTGCATCC 835

RESULT 2
CF147821

LOCUS CF147821 704 bp mRNA linear EST 25-JUL-2003
DEFINITION AGENCOURT 14740195 NIH MGC 145 Homo sapiens cDNA clone
IMAGE:6971900 5', mRNA sequence.
ACCESSION CF147821
KEYWORDS CF147821.1 GI:33244089
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: IRB102 row: b column: 07
High quality sequence atop: 685.
Location/Qualifiers

FEATURES

source

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/clone="IMAGE:6971900"
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/clone_1lb="NIH_MGC_145"
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmiI/XhoI-3', 5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/fearrayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1,696-72 Length: 704
Score: 806.50 Matches: 151
Percent Similarity: 81.25% Conservative: 31
Best Local Similarity: 67.41% Mismatches: 41
Query Match: 39.61% Indels: 1
DB: 7 Gaps: 1

US-10-626-398-10 (1-389) x CF147821 (1-704)

5 AanserThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
11 AATAGACAAATCAATTTATTCACAGACACTCGTGTACTTTCAGATTTTATGTCCTTA 70
24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
71 GTAGCTTTTGTCTAATATGCTAGAAATGCTTGTGTCATTTTACCTTTGTGTGACAAA 130
44 AenLeuArgHisArgSerAsnTyrrPheLeuAsnLeuAlaIleAlaAspPheVal 63
131 AACCTTAGACATCGAAGTAGTATTTTCTTAACTTGCCCATCTCTGACTCTTTGG 190
64 G1yAlaIleAlaIleProLeuTyrrIleProSerSerLeuThrTyrrPheSerGlyLys 83
191 GGTGGATCTTCATCTCTTGTATACATCCCTCACACAGCTTTGGAATGGATTGGAAAG 250

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 721)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB18 row: a column: 04
High quality sequence start: 2
High quality sequence stop: 328.
Location/Qualifiers

FEATURES

source

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/notes="Vector: pCDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.llnl.gov/image.rearrayed_plates/IRBF.presv.dat
a. Note: this is a NIH-MGC library."

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ORIGIN

Alignment Scores:

Pred. No.:	5,966-35	Length:	721
Score:	443.50	Matches:	87
Percent Similarity:	80.77%	Conservative:	18
Best Local Similarity:	66.92%	Mismatches:	24
Query Match:	21.78%	Indels:	1
DB:	7	Gaps:	1

US-10-626-398-10 (1-389) x CO959034 (1-721)

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OY 5 AensertThlleleleuThr---SerlelySleSerleuThrPheteuMetSerleu 23
    |||||
DB 34 AATAGACAAATTAATTAATCACTAGACACTCGGTACTTGAATTTTATGTCCTTA 93
    |||||
OY 24 leualailealeleuThrleuGlyAenValValleleuAlpheleValaspar 43
    |||||
DB 94 GTAGCTTTGCTATATAGTAGGAATGCTTTGCTATTTAGCTTTGTGAGCAAA 153
    |||||
OY 44 AenleuAghAargSerAntyrPhePheleuAenleuAlleleAlasPhePheVal 63
    |||||
DB 154 AACCTTAGACATGAAAGTATTTTCTTAATCTTGCCATCTGATCTTCTTG 213
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OY 64 GYAAlleleAllelePheleuTyrlleProserSerleuThrTyTrpPhserGlylys 83
    |||||
DB 214 GGTGATCTCCATTCCTTTGATACCTCTCACGCTTTGGAATGGGATTTGAAAG 273
    |||||
OY 84 GlnAlaCyValPheTrpPheleuThraSPYrleuLeuCyThraLaseValTyraen 103
    |||||
DB 274 GAAATCTGTATTTTGGCTCACTGATCTATCTGTTATGTAACGACATGATTAAG 333
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OY 104 llealleuIleSerTyraSPargTyrgInSerValSerAenAlaValTrpTyraAla 123
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DB 334 ATTGCCATCAGCTATGATATAAATCGTCAATCTGATTAATGCTTGTATGAAAG 393
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OY 124 GlnHISerglyThrTrpylelleleuThr 133
    |||||
DB 394 CAAAAACGGGGGCGCTGAAGGGGAACG 423
    |||||

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RESULT 5
AY400784
LOCUS
DEFINITION
Mus musculus CHRM3 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY400784
ACCESSION
AY400784.1 GI:39756773
VERSION
KEYWORDS
SOURCE
GSS.
ORGANISM
Mus musculus (house mouse)

REFERENCE

AUTHORS

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers

FEATURES

source

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ORIGIN

Alignment Scores:

Pred. No.:	2,716-30	Length:	1770
Score:	404.50	Matches:	131
Percent Similarity:	40.00%	Conservative:	83
Best Local Similarity:	24.49%	Mismatches:	138
Query Match:	19.87%	Indels:	183
DB:	9	Gaps:	19

US-10-626-398-10 (1-389) x AY400784 (1-1770)

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OY 15 lleSerleuThrPheteuMetSerleuAenleuAlleleleuGlyAenValVal 34
    |||||
DB 202 GCTTCATTCGATCTTTTATCGCTTCTCGGATTTGGTGAACCATGCGCAATCCTT 261
    |||||
OY 35 ValIleleuAlpheleValasparAenleuAghAargSerAntyrPhePheleu 54
    |||||
DB 262 GTCATTTGGCATTTAAGTCAACAAGCGTGAAGACGTGAACACTTCCCTTA 321
    |||||
OY 55 AenleuAlleleAlasPhePheValGlyAlleleAllelePheleuTyrlleProser 74
    |||||
DB 322 AGCTGCGCTGGCGAGATCTGATCTCGGGGTCATTTCCATGAACCTGTC----- 372
    |||||
OY 75 SerleuThrTyr-----TrpHISerglyGlnAlaCyValPheTrp 89
    |||||
DB 373 --ACGACCTACATCATTAATGAACCGCTGGGCTCGGGAACTTAAGCTGACCTTGG 429
    |||||

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QY	90	LeuLeuIeHApPryrLeuLeuCyethrAlaSerValTyrAsnIleValIleuIleSerTyr	109
DB	430	CTTTCACATGACATATGAGCCAGCAAGCTCTCTGATCATGAATCTGCTGGATACAGCTTT	489
QY	110	AspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAlaGlnHisSerGlyThrTrp	129
DB	490	GACAGTACTTTCTTATATACCAAGGCACCTTACCGAGCCAAACGA-----ACAA	543
QY	130	LyAlIeAlaThrGlnMetValAlaVal---TrpIlePheSerPheMetThrAsnGlyPro	148
DB	544	AAAGAGACCGGGTGTGATGATTGTCCTGGCTTGGGGCATCTCTTGTCTGTGGAGCTCT	603
QY	149	MetIleLeuIleSerAspSerTrpGlnAsnSerThrThr-----GluCysGlu	164
DB	604	GCCATCTCTGTTCTGGCAATACTTTGTAGGAAGAAGACTGTGCCCCCGGAGAAATGTTTC	663
QY	165	ProGlyPheLeuLysIleTyrTrpPheAlaLeuProThrSerLeuLeuGluPheLeuIle	184
DB	664	ATTCAAGTTTCTAATGAGAGCCACCATCATCTTCGGACGGGAGTGGCTGCTTTTACATG	723
QY	185	ProIleLeuLeuValAlaIaIaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg---	203
DB	724	CTGTGCACCATCATGACTATT-----TTATACTGAGAGATATATTAAGAGACT	771
QY	204	GluIlyLeuSerArgCysLeuSer-----	211
DB	772	GAGAAACGTACAAAGAAGCTGTGCTGGCTACAGGCTCTGGAGACAAAGCGAAGACAGA	831
QY	212	-----HisProValLeuProSerAspSerSerSerSer-----	222
DB	832	AACTTTGTCCACCCACAGGAGTTCTGAAGCTGTAGACACTATAGACTTAACAAGCAA	891
QY	222	-----	222
DB	892	GGCAGGAACGCTATCTAGAGAGAAGTATGCTGCTGTCTCATCTTGTGTTCAACTAAG	951
QY	223	-----AspHisGlyHisSerCysArg-----Gln	230
DB	952	AGCTGGAAGCCAGCTGTGACAGCATGTGACCAAGCACACATAGACATGACATGTGGAA	1011
QY	231	AspProAspSerArgAlaIaThrLeuProAlaArgLysGluThrThrAlaSer-----	247
DB	1012	AACACGATGCTGCTGCTCTCCCTG-----GAAAACCTGTGCTTCTTGATGAA	1059
QY	248	-----LeuGlyIleSerAsp-----	251
DB	1060	GAGATATATGCTGTGAGACAGACAGACCATTAATTCATTGATACCAAGCTGCCGGGTAT	1119
QY	252	LysSerIleArgLysIleSerSerLeuLeuProSer-----	262
DB	1120	AGCACCATCTCAACTCTTAACCAAGTACCTCTTCAGATAACTGTGAGTGCACAGACAAG	1179
QY	263	-----IleArgAlaTyrLys-----	267
DB	1180	GACCTGGGAGCTATATGATGTATAGAGAAATGCCCTTAAGCTTCAAGGCCCAAGAAAGTATG	1239
QY	267	-----	267
DB	1240	GATGACCGTGACAACTGTCAAGAGACTTCTCAAGCTCCCATTCACAGTTAGAGCTTGC	1299
QY	268	-----AsnSerIleVal-----	271
DB	1300	GTGACACAGACCAAGACTCTTGACACCAACTCTCTGGTGGACAGACCAAGCCGCTTTA	1358
QY	272	-----IleIleSerIleAsnGlyPheLeuSerHisSerAsp	283
DB	1360	CCTGTGCTCTCAAGAGAACCAAGCTGTGCTAAGAGTGTGCTCTCAAGACCAAGATGAG	1419
QY	284	SerLeuAlaLeuGlnIleArgLysIleIleGluLeuPheArgAlaArgLysLeuAlaLys	303
DB	1420	-----ATCACCAAGCGGAAAGATGTGCTCATCAAGAGAAAGAAAGCGCCGACG	1470

[illegible]


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QY 267 ----- 267
Db 2024 GATGACCGTGACAACCTGTGAGAGACTTCTCCAGCTCCCATCCAGTTAGAGTGTGCC 2083
QY 268 -----AenSerAsnVal1----- 271
Db 2084 GTGACACAGACCAAGACTCTGTGACACCAACTCTCGGTGGACAAGACCAAGCGCGCTTA 2143
QY 272 -----1leAlaserLyemecLylpheuSerHisSerAp 283
Db 2144 CCTGTGCTCTTCAGAGACCGACGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTG 2203
QY 284 SerLeuAlaLeuGlnGlnArgGlnHisLeuLeuPheArgAlaArgLySerLeuAlaLys 303
Db 2204 -----ATCACCAAGCGGAAAGAGATGCTGCTATCAAGAGAAAGAGCGCCGCG 2254
QY 304 SerLeuAla1leLeuLeuAla1a1aPheAla1a1eCysTrpAlaProTyrSerLeuThr 323
Db 2255 ACACGACGAGCCATCTTGTGCTGCTTGTGCTTGTGCTGACGCGCCCTACAAACATCATGTC 2314
QY 324 Val1leTyrSerPhePheProGlnArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343
Db 2315 CTGGTGACACACCTTCTGTGAC-----AGCTGCATACCCAAACCTATTGGAATCTGGC 2368
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
Db 2369 TACTGCTGTGCTATATCAACAGCAGCCGTAACCCGCTGTGCTATGCTGCTGCTGCAACAG 2428
QY 364 ArgPheGlnLysAlaPheLeuLys1leLeuProVal----- 375
Db 2429 ACATTGACAACCACTTCAAGATGCTTCTTATGCGACAGTGACAAAGAGAGAGCGCGC 2488
QY 376 -----ArgArgGlnSerThrProProHisAsnArg 385
Db 2489 AAACAGCAGTACCAAGACAGACAGTCCGTCATTTCACAAAGGA 2533

RESULT 7
AY400782 1773 bp DNA linear GSS 15-DEC-2003
LOCUS Homo sapiens CHRM3 gene, VIRUTUAL TRANSCRIPT, partial sequence.
ACCESSION AY400782
VERSION AY400782.1 GI:39756771
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1773)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..1773
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1773
gene

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ORIGIN
Alignment Scores:
Pred. No.: 3,45e-30 Length: 1773
Score: 403.50 Matches: 129
Percent Similarity: 39.254 Conservative: 79
Best Local Similarity: 24.344 Mismatches: 152
Query Match: 19,828 Gaps: 14
DB: 9

US-10-626-398-10 (1-389) x AY400782 (1-1773)
QY 15 1leSerLeuThrPheLeuMetSerLeuLeuAla1a1a1leMetLeuGlnLysAsnVal 34
Db 205 GTCTTCATGCTTCTTCAAGCGGACATCGCGCTTGGTGAACCATCATCGCAACATCTG 264
QY 35 Val1leLeuAlaPhe1leValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeu 54
Db 265 GTTATTGTGCTATTAAAGTCAACAGCAGCTGAACGCGTGAACAACACTTCTCTTA 324
QY 55 AsnLeuAla1leAlaAspPhePheValGlyAla1a1a1leProLeuTyrIleProSer 74
Db 325 AGCTGCGCTGTGCGCATCTGATTATCGGGGTCATCATGAATCTGTTT----- 375
QY 75 SerLeuThrTyr-----TrrPheSerGlyLysGlnLysValPheTyr 89
Db 376 ---ACGACCTTACATCATCATGAATCGATGCGCTTGAAGAACTTGCGCTGTGACCTTG 432
QY 90 Leu1leThrAspTyrLeuLeuCysThrAlaSerValTyrAsn1leValLeu1leSerTyr 109
Db 433 CTTCGATGACTAGCTAGTACCAAGCAATGCTCTGTTATGAATCTTGATCATCACTT 492
QY 110 AspArgTyrGlnSerValSerAsnAlaVal1TrrPyrArgAlaGlnHisSerGlyThrTyr 129
Db 493 GACAGATACCTTTCATCCACAGAGCGCGCTGACGTAACGCAACGA-----ACAA 546
QY 130 Lys1leAla1leThrGlnMetValAlaVal---TrrIlePheSerPheMetThrAsnGlyPro 148
Db 547 AAGAGAGCGGTGTGTATCGCTGCGTGGCTGCTGCTTGTGCTTGTGCTTGTGCTGCT 606
QY 149 Met1leLeu1leSerAspSerTrrPheAsnSerThrThr-----GlyCysGlu 164
Db 607 GCCATCTTGTGCTGCAATCATCTTGTGGAAGAGAACTGCTCCGCGGAGAGTCTTC 666
QY 165 ProGlyPheLeuLysLysTrrPyrPheAlaLeuProThrSerLeuLeuGlnPheLeu1le 184
Db 667 ATTCACTTCTCAGTGAAGCCACCATTAATTGTCGACAGCCATCGCTGCTTTTATATG 726
QY 185 Pro1leLeuLeuValAlaTyrPheSerAlaHis1leTyrTrrSerLeuTrrLys----- 202
Db 727 CCTGTCAACCATATGACTATT-----TTTACTGAGGATCTATTAAGAAACT 774
QY 202 ----- 202
Db 775 GAAAAGCGTACCAAGAGCTTGCTGCTGCAAGCTCTTGAGACAGAGCAGACAGAA 834
QY 202 ----- 202
Db 835 AACTTGTCCACCCCGGAGGAGTTCTCGAAGTGCAGAGTTACGAACTTCAACAGCAA 894
QY 203 -----ArgGlyLysLeuSerArgCys----- 209
Db 895 AGCATGAAACGCTCCAAACAGAGAGAGTATGCGCTGCACTTCTGTTCACAAACAG 954
QY 210 -----LeuSerHisProValLeuProSerAspSerSerSerAspHis-GlyHis 226
Db 955 AGCTGAAACCCAGCTCCGACAGATGACCAAGACCAACAGCAGCAGTACAGTGAAC 1014
QY 226 sSerCys-----ArgLysProAspSerArgAlaThrLeu-- 238
Db 1015 AACCAATGATGCTGCTGCTGCTGAGAACTCGCGCTCTCGACGAGAGAGACATTGGC 1074

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Qy	239	ProAlaArglypsgiuThrThrAlaSerLeuGlySerAspIysSerArgArglySerSer	258
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Qy	258	rLeuLeuProSerIleArgAlaTyrIlyAsnSerAsnValIleAlaSerIlyMetGlyPh	278
Db	1135	AACTCCACCAAGTTACC-TCATCGGACCAACCTGCAGGTGCTGAGAGGAGCTGGGAT	1193
Qy	278	eLeuSer-----HisSerAspSerLeuAlaLeuGln-----	288
Db	1194	GGTGGACTTGGAGAGAAAGCCGACAGCTGCAGGCCCAAGAGCCTGCAGATTGAGG	1253
Qy	288	-----	288
Db	1254	CAGTTTCCAAAAAGCTTCTCCAAAGCTTCCATCCAGCTAGAGTCAGCCGTGACACAGC	1313
Qy	288	-----	288
Db	1314	TAAGACTTGTAGCGTCAACTCTCAGTGGTAAGACAGCGCCACTTACTCTGTCTT	1373
Qy	289	-----GlnAr	290
Db	1374	CAAGAAAGCCACTGTGGCCAAAGGTTGTCTGTGAAGCCAGAACTCAGATCACTAAAGC	1433
Qy	290	gGluHisIleGluLeuPheArgAlaArgIlyLeuAlaIlySerIleuAlaIleLeuLeuAl	310
Db	1434	GAAAGAGATGTCCTCGTGCATCAAGAGAAAGAAAGCGGCCAGACCTCATGTGGATCTT	1493
Qy	310	aAlaPheAlaIleCysTrpAlaProTyrSerLeuThrValIleTyrSerPhePhePr	330
Db	1494	TGCCTTCACTACACTTGGAGCCCAACATCACTCATGTCTCTGGGAACACCTTTGTGA	1553
Qy	330	oGluArganLeuThrIlySerThrTyrHisThrAlaPheIleuGlnTrpPheAs	350
Db	1554	C-----AGTCGATACCAACCAAAACCTTTGGATCTGGGACTACGCTGTGCTCATCA	1607
Qy	350	nSerPheAlaIleProPheLeuTyrProLeuCysHisIlyAsnArgPheGlnIlyAlaPheLe	370
Db	1608	CAGCACCGGTGAACCCCGTGTGCTATGCTGTGCAAAACAAATTCAGAACCACTTTC	1667
Qy	370	uIyelleLeuProVal-----ArgAr	377
Db	1668	GATGCTGTCTGCTGTGCCAGCTGACAAAAAAGAGGGCGCAAGCAGCTACCAAGCAG	1727
Qy	377	gGlnSerThrProProHisIleAsnArgSer	386
Db	1728	ACAGTCGCTCATTTTTCACAAAGCGCGCA	1755
RESULT 8			
LOCUS	AK032763	2780 bp	mRNA linear HTC 03-APR-2004
DEFINITION			mus musculus 12 days embryo male wolffian duct includes surrounding
			region cDNA, RIKEN full-length enriched library, clone:672043D06
			product: HISTAMINE RECEPTOR H1, full insert sequence.
ACCESSION	AK032763		
VERSION	AK032763.1	GI:26328544	
KEYWORDS	HTC; CAP trapper		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Wich. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
	Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
	Normalization and subtraction of cap-trapper-selected cDNAs to		
	prepare full-length cDNA libraries for rapid discovery of new genes		
TITLE			

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	Genome Res. 10 (10), 1617-1630 (2000) 20499374 11042159 3
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,F., Komoto,H., Akiyama,J., Nishi,K., Kiteunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Mashino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakauechi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Macnura,S., Kawai,J., Okazaki,T., Mizumatsu,M., Inoue,Y., Kita,A., and Hayashizaki,Y. RIKEN Integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000) 11076861 4
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 5
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2780) Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,F., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hoti,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Komno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohnato,N., Okazaki,Y., Saito,R., Saitoh,K., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Saeki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yaeunishi,A., Muramatsu,M., and Hayashizaki,Y. Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/ Location/Qualifiers 1. .2780 /organism="Mus musculus" /mol_type="mRNA" /retail="C57BL/6J" /db_xref="FANTOM_DB:6720430L06" /db_xref="taxon:10090" /clone="6720430L06" /sex="male" /tissue_type="wolfian duct includes surrounding region" /clone_id="RIKEN full-length enriched mouse cDNA library" /dev_stage="12 days embryo" 70. .1536 /note="unnamed protein product: HISTAMINE RECEPTOR H1 (SPRR19)1V75, evidence: FASTY, 100%ID, 100%length, match=1464) putative"
CDS	

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ORIGIN

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Alignment Scores:
Pred. No.:      1.01e-29      Length:      2780
Score:          402.00      Matches:      117
Percent Similarity: 41.44%      Conservative: 84
Best Local Similarity: 24.12%      Mismatches: 164
Query Match:     19.74%      Indels:      120
DB:              3          Gaps:      14

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US-10-626-398-10 (1-389) x AK032763 (1-2780)

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QY      21 MetSerLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIle 40
DB      169 CTAAAGTAGTATCCCTCGTCACAGTGGGCTCAACTGCTGGTGCTGTATGACGTCGC 228
QY      41 ValAspArgAsnLeuAlaGlyHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAsp 60
DB      229 AGTGAGGCAAGCTACACACCTGGGCACTGTGACCTTGTCACTGCTGGTAGCGAC 288
QY      61 PhePheValGlyAlaIleAlaIlePro-----LeuTyrIleProSerSerLeuThr 77
DB      289 CTGATTGTAGGGGAGCGATCGTCATGCCCATGAACATCTCTTATCTT-----ATCATAC 342
QY      78 TyrTyrPheSerGlyLysGlnAlaCysValPheTyrPheLeuIleThrAspTyrLeuLeuCys 97
DB      343 AAGGTGCTCGTGGCGCGCCCGCTGCTCTTTGGCTGTCTATGATTAATGTCGACG 402
QY      98 ThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsn 117
DB      403 ACGGCATCCATCTTACTGTCTTCATCTGTATGATGCTACCGCTGTGTCACGAA 462
QY      118 AlaValTyrPyrArgAlaGlnHisSerGlyThrTyrPyrIleAlaThrGlnMetValAla 137
DB      463 CCCCTCCGGTACTGAGGTATCGAACCAGACCCGCTTCACTACCC-----ATCTGCGG 519
QY      138 ValTyrIlePheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTyrGln 157
DB      520 GCGCGGTTCTCTCCCTTCTGCGGTATACCTTACTT-----GCGTGGCAT 567
QY      158 AsnSerThr-----ThrGluCysGluProGlyPheLeuLys 169
DB      568 CACTTCACGCGCCCTGCGCCAGAGCTTCGGGAGAGATAGTGAGACAGATTCTTACAT 627
QY      170 LysTyrPyrPheAlaLeuProThrSerLeuLeuGluPheLeuIleProIleLeuVal 189
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QY      190 AlaTyrPheSerAlaHisIleTyrTyrSerLeuTyrPyrArgGluLysLeuSerArgCys 209
DB      688 CTGGGTTCATATGAGATCTACAGGCTGTG---CGGCGACACTGTACACCGCGCAG 744
QY      210 LeuSerHisProValLeuProSer----- 217
DB      745 CTCACCAACGGGCTCTCCCTCTTTTGAATAATCAAGCTGAGGTGGAGATGCCAA 804
QY      218 -----AspSerSerSerSerAspHisGlnHisSerCysArg-----Gln 230

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DB      805 GAGGGTGCCAAAGAACTGGGAAAGAGTCTCCCTGGGGGGGTCCAGAAAGAGCGGCTCAAGA 864
QY      231 AspPro-----AspSerArgAlaThrLeuProAlaArgLysGluThrThrAla 246
DB      865 GACCTCACTGAGAGTGTGTGATCGAAAGTCAACATCTGAAAGACCCCAAGGTGACCTTCCG 924
QY      247 SerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIleArg----- 264
DB      925 ACTGTCTTCAAGCAAGAGGGGAAAGGAAAGCAAGTCAACAGCCCTTCTTCCGTTTGAC 984
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DB      1045 ACCTTGAGCCAGCCCAAAATGATGAGCAGAGCCTGATCTTCCGCGGATCACTGAG 1104
QY      266 TyrLeuAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAspSer--- 284
DB      1105 ACATCAGAGACCAAGACCTTGTGTGATGCACAGTCTTCTCCCGACACACAGACTCAGAC 1164
QY      284 ----- 284
DB      1165 ACCAGCATGAGCGCAGGGCTGGGCAAGTCAAGCGAGACAGAGCTTAACAGTGGCTG 1224
QY      285 -----LeuAlaLeuGlnGlnArgGluHisIle----- 293
DB      1225 GACTACATCAAGATGACCTGGAAAGGCTCCGCTCACTTCCAGACAGTGTGTGTCGGG 1284
QY      294 ---GluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuAlaAlaPhe 312
DB      1285 TTGCACCTTGAAACGAGAGCGGAAAGCAGCCAGACAGATGGAGTTGATCATGCGACATTC 1344
QY      313 AlaIleCysThrAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
DB      1345 ATTCTGCTGCGATTCCTCATTTTCATCTTCTCATGTGATGTGATGCTTCTGCTG 1395
QY      333 AsnLeuThrLysSerThrTyrTyrHisThr---AlaPheThrLeuGlnThrPheAsnSer 351
DB      1396 AACAGCTGTGCGACGGAACCTGTGCACATGTGCACCATTTGGGTGGCTCATCACTCC 1455
QY      352 PheValAsnProPheLeuTyrProLeuCysHisLysAlaArgPheGlnLysAlaPheLys 371
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QY      372 IleLeuProValArg 376
DB      1516 ATTCTGACATTCGT 1530

```

RESULT 9

AK047070 2831 bp mRNA linear HTC 03-APR-2004
 LOCUS AK047070
 DEFINITION Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length
 enriched library, clone:B930016C09 product:HISTAMINE RECEPTOR H1,
 full insert sequence.

ACCESSION AK047070
 VERSION AK047070.1 GI:26338557
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE

1. Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE
Normaliza-tion and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159
REFERENCE
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., et al.

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Qy 218 -----AepSerSerSerAspHisGlyHisSerCysArg-----Gln 230
Db 908 GAGGTCGCCAAGAACTGGGAAAGACTCTCCCTGGGGGGTCCGAAGAGCCCTCAGA 967
Qy 231 AapPro-----AapSerArgAlaThrLeuProAlaArgGlyGluThrAla 246
Db 968 GACCCTACTGGAGGTCTGATCAGAACATCTGAAGACCCCAAGGTGACTCTCCG 1027
Qy 247 SerLeuGlySerAspIysSerArgArgIysSerSerLeuProSerIleArg----- 264
Db 1028 ACTGCTTTCACCAAGGGGGAAGGAAACAGTCAACGCGCCCTGTTCCGTTCGAC 1087
Qy 264 ----- 264
Db 1088 GTCATGACAGACAGCCTGTGCTCGAGGAGATGCCAGGGGCTCAAGGCCATGACCAG 1147
Qy 265 -----Ala 265
Db 1148 ACCTTGAGCAGCCCAAAATGATGACAGAGCCTGACTTCCGCGGATCATGTAG 1207
Qy 266 TyrllysAsnSerAsnValIleAlaSerIysMetClyIleLeuSerHisSerAapSer--- 284
Db 1208 ACATCAGAGAGACGACCTTGAGTGCACAGTCTTTCGCCGACACAGACTCAGAC 1267
Qy 284 ----- 284
Db 1268 ACCAGCATAGAGCCAGGGCTGGGCAAGTCAAGCCGAAGCAGGTCAACAGTGGCCTG 1327
Qy 285 -----LeuAlaLeuGlnIleArgGluHisIle----- 293
Db 1328 GACTACATCAAGTCACTGGAGAGAGGCTCGGCTCACATTCACAGACAGTATGTCTCCGG 1387
Qy 294 ----GluLeuPheArgAlaArgIysLeuAlaIysSerLeuAlaIleLeuAlaIleAlaPhe 312
Db 1388 TTCACCTTGAAACCGAGCGGAAAGGACGCAAGAGTGGTGTATCAGCAGCAGCATTC 1447
Qy 313 AlaIleCysTrpAlaProIysSerLeuThrValIleIysSerPhePheProGluArg 332
Db 1448 ATTCTCTGCTGGATCCCTATTTCATCTTCTTCATGTCATGCTTCTGCG----- 1498
Qy 333 AsnLeuThrIysSerThrTrpIysIleThr---AlaPheTrpLeuGlnTrpPheAsnSer 351
Db 1499 AACAGCTGTGACGCAAGCTGTGCATGTCATGTCATTTGGCTGGGCTCATCACTCC 1558
Qy 352 PheValAsnProPheLeuIyrProLeuCyHisIysArgPheGlnIysAlaPheLeuIys 371
Db 1559 ACCGTGAACCCCTCATCTACCCGCTGTGCACGAGAACTTCAAGAGACATTCAAAAA 1618
Qy 372 IleLeuProValArg 376
Db 1619 ATTCTGCACATTGCT 1633

RESULT 10
AK038480 2979 bp mRNA linear HTC 03-Apr-2004
LOCUS AK038480
DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length
enriched library, clone:A230019E03 product:HISTAMINE RECEPTOR H1,
full insert sequence.
ACCESSION AK038480
VERSION AK038480.1 GI:26312590
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.

REFERENCE
1 Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL 99279253
MEDLINE 10349636
PUBMED 2
REFERENCE
2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

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TITLE
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MEDLINE
PUBMED
REFERENCE
AUTHORS

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PUBMED
REFERENCE
AUTHORS

COMMENT
CDS
FEATURES
source

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Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159
 3
 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
 Konno,H., Akiyama,J., Nishi,K., Kitsuina,T., Tashiro,H., Itoh,M.,
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
 Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M.,
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsumura,S., Kawai,J.,
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
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 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5
 The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 2979)
 Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,N.,
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
 Muramatsu,M. and Hayashizaki,Y.
 Direct Submission
 Submitted (16-Jul-2001) Yoshihide Hayashizaki, The Institute of
 Physics and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.jp,
 url:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
 Fax:81-45-503-9216)
 CDS
 CDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL:http://genome.gsc.riken.jp/
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ORIGIN

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Query Match:	19.74%	Indels:	120
DB:	3	Gaps:	14

US-10-626-398-10 (1-389) x AK03480 (1-2979)

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QY      41 ValAspArgAsnLeuArgHisArgSerAntYrPhePheLeuAsnLeuAlaIleAlaAsp 60
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QY      78 TyrTrpThrSerGlyLysGlnAlaCyValPheTrpLeuIleThrAspTyrGlnSerVal 97
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DEFINITION full insert sequence.
ACCESSION AK046607
VERSION AK046607.1 GI:26338238
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
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REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itch, M., Komu, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
AUTHORS		Normalization and subtraction of cap-trapper-selected cDNAs to
TITLE		prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL		Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE		20499374
PUBMED		11042159
REFERENCE	3	Shibata, K., Itch, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komu, H., Akiyama, J., Nishi, K., Kitanai, T., Tashiro, H., Itch, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisake, S., Inoue, K., Togawa, Y., Iwawa, M., Ozara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
AUTHORS		RIKEN integrated sequence analysis (RISA) system--384-format
TITLE		sequencing pipeline with 384 multiplexed sequencer
JOURNAL		Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE		20530913
PUBMED		11076861
REFERENCE	4	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
AUTHORS		Functional annotation of a full-length mouse cDNA collection
TITLE		Nature 409, 685-690 (2001)
JOURNAL		5
REFERENCE		The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
AUTHORS		Analysis of the mouse transcriptome based on functional annotation
TITLE		of 60,770 full-length cDNAs
JOURNAL		Nature 420, 563-573 (2002)
REFERENCE		6 (bases 1 to 3783)
AUTHORS		Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fuyuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, P., Imocani, K., Ishii, Y., Itch, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komu, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Satoh, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaki-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
JOURNAL		Direct Submission
TITLE		Submitted (16-JUL-2001) Yoshihide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-research@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT		cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES		Please visit our web site for further details.
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Rattus.
REFERENCE 1 (bases 1 to 672)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1401)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1401)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submision
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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DB: 9 Gaps: 16
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Qy      284 SerLeuAlaLeuGlnGlnArgLuhisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
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Db      994 GAGTTTCAAGAAAGCCTTTTCAGAATGTGCTGCCAATCATCATGCTTCGCGAAGGCA 1053
Qy      380 Thr 380
Db      1054 TCC 1056

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RESULT 15
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LOCUS      AK085653
DEFINITION      Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched
                  library, clone: D630050N06 product: adrenergic receptor, alpha 1a,
                  ALPHA 1A-ADRENOCEPTOR, full insert sequence.
ACCESSION      AK085653
VERSION      AK085653.1 GI:26351716
KEYWORDS      HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1

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AUTHORS      Carninci, P. and Hayashizaki, Y.
TITLE      High-efficiency full-length cDNA cloning
JOURNAL      Meth. Enzymol. 303, 19-44 (1999)
MEDLINE      99279253
PUBMED      10349636
REFERENCE      2
AUTHORS      Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
                  Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE      Normalization and subtraction of cap-trapper-selected cDNAs to
                  prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL      Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE      20499374
PUBMED      11042159
REFERENCE      3
AUTHORS      Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
                  Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
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                  Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
                  Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
                  Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J.,
                  Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE      RIKEN integrated sequence analysis (RISA) system--384-format
                  sequencing pipeline with 384 multiplexed sequencer
JOURNAL      Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE      20530913
PUBMED      11076861
REFERENCE      4
AUTHORS      The RIKEN Genome Exploration Research Group Phase II Team and the
                  FANTOM Consortium.
TITLE      Functional annotation of a full-length mouse cDNA collection
JOURNAL      Nature 409, 685-690 (2001)
MEDLINE      11076861
PUBMED      11076861
REFERENCE      5
AUTHORS      The FANTOM Consortium and the RIKEN Genome Exploration Research
                  Group Phase I & II Team.
TITLE      Analysis of the mouse transcriptome based on functional annotation
                  of 60,770 full-length cDNAs
JOURNAL      Nature 420, 563-573 (2002)
MEDLINE      12000000
PUBMED      12000000
REFERENCE      6
AUTHORS      Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
                  Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
                  Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
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                  Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
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                  Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohnishi, N.,
                  Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
                  Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
                  Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S.,
                  Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
                  Muramatsu, M. and Hayashizaki, Y.
TITLE      Direct Submission
JOURNAL      Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
                  Physical and Chemical Research (RIKEN), Laboratory for Genome
                  Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
                  RIKEN Yokohama Institute, 1-7-22 Suhei-cho, Tsurumi-ku, Yokohama,
                  Kanagawa 230-0045, Japan [E-mail: genome-res@gs.c.riken.jp,
                  URL: http://genome-gsc.riken.jp/, Tel: 81-45-503-9222,
                  Fax: 81-45-503-9216]
COMMENT      cDNA library was prepared and sequenced in Mouse Genome
                  Encyclopedia Project of Genome Exploration Research Group in Riken
                  Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                  Division of Experimental Animal Research in Riken contributed to
                  prepare mouse cDNAs.
                  Please visit our web site for further details.
                  URL: http://genome-gsc.riken.jp/
                  URL: http://fantom.gsc.riken.jp/
                  Location/Qualifiers
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Score: 391.00 Matches: 117
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Best Local Similarity: 29.18% Mismatches: 139
Query Match: 19.20% Indels: 84
DB: 3 Gaps: 16

US-10-626-398-10 (1-389) x AK085653 (1-4124)

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QY 24 -----LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPhe 39
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QY 40 IleValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAlaIleAla 59
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QY 60 AspPhePheValGlyAlaIleAlaIleProLeu---TyrIleProSerSerLeuThrTyr 78
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QY 79 TrpThrSerGlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThr 98
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DB 1286 GCGTCCATCGAGGCTCTGCATCATCTCATCGACCGATACATGTGTGAGCTACCG 1345
QY 119 ValTrpTyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGln----- 134
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QY 135 -----MetValAlaValTrpIlePheSerPheMetThrAsn---GlyProMetIleLeu 151
DB 1385 AGGGCTCTGCTGCTGGGCGCTTCTTGCTCATCTCCATCGGACCCCTGCTC--- 1441
QY 152 IleSerAspSerTyrGlnAsnSerThrThrGlu-----Cys----- 163
DB 1442 -----GCTGGAGGACGACAGGCTCCGGAGGATGAGACCATCTGCAATCAATGAG 1492
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DB 1493 GACCCAGATACGTG-----CTGTTCTACAGCGTGGGCTCTTCTAC 1534
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DB 1535 GTGCCACTGACCACTATCTGTTATGATCTGTCGAGCTAC---GTGGTAGCCAAAGAGA 1591
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 1592 GAA-----AGCCGAGGCTCAAGTCCGG---CTCAAGACCAAGTAGACTCAGAG 1642
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
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QY 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
DB 1670 AATGTCCTGCAGAAAGCAGCGGAGTGAAGCAGTGCAGAAATAGACTCACTTCTCGTG 1729
QY 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
DB 1730 AGGCTGCTCAAGTTTTC----- 1747
QY 284 SerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
DB 1748 -----CGAGAGAAAGAAAGCGCCAG 1768
QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
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QY 380 Thr 380
DB 2006 TCC 2008

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 01:44:58 ; Search time 172 Seconds

(without alignments)
1158.133 Million cell updates/sec

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Perfect score: 2036
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2025	99.5	389	2	Q91ZY3
2	1310.5	64.4	390	2	Q96LD9
3	1308.5	64.3	390	1	HH4R_HUMAN
4	1244	61.1	391	2	Q91ZT2
5	1235.5	60.7	391	2	Q91ZT1
6	1221.5	60.0	390	2	Q8WNV9
7	693	34.0	445	1	HH3R_CAVPO
8	689.5	33.9	445	1	HH3R_HUMAN
9	688.5	33.8	445	2	Q86SE1
10	681.5	33.5	445	1	HH3R_RAT
11	679.5	33.4	445	1	HH3R_MOUSE
12	666	32.7	473	2	Q6ZM33
13	655.5	32.2	365	2	Q8WY01
14	655.5	32.2	373	2	Q8WY02
15	534.5	26.3	174	2	Q6J9J4
16	528.5	26.0	175	2	Q6J9J5
17	472	23.2	301	2	Q8WY00
18	472	23.2	309	2	Q8N149
19	414	20.3	639	1	ACM3_CHICK
20	413.5	20.3	590	1	ACM3_BOVIN
21	413	20.3	585	1	ACM3_CARTEL
22	410	20.1	486	1	HH1R_RAT
23	408.5	20.1	589	1	ACM3_RAT
24	407.5	20.0	528	2	Q9PTF6
25	406	19.9	488	1	HH1R_CAVPO
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28	404	19.8	488	2	Q91V49
29	403.5	19.8	590	1	ACM3_GORGO
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33	402.5	19.8	531	1	ACM5_RAT	P08911 ratius norv
34	402	19.7	488	1	HH1R_MOUSE	P70174 mus musculu
35	402	19.7	488	2	Q91V66	Q91v66 ratius norv
36	402	19.7	564	2	Q96RG9	Q96rg9 homo sapien
37	400	19.6	611	2	Q7JRV1	Q7jrv1 caenorthabdi
38	399	19.6	587	2	Q8VH26	Q8vh26 cavia porce
39	395.5	19.4	487	2	Q9N2B1	Q9n2b1 gorilla gor
40	395.5	19.4	532	1	ACM5_HUMAN	P08912 homo sapien
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42	394.5	19.4	530	2	Q8VH24	Q8vh24 cavia porce
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ALIGNMENTS

RESULT 1

ID Q91ZY3 PRELIMINARY; PRT; 389 AA.

AC Q91ZY3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Histamine H4 receptor.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]

RP SEQUENCE FROM N.A.

RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF358858; AAK97379.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPSN.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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QY	121	YRQSHGWTWIAIQMAVWVLFSPFTMGPMILISDSWQNSTTECEPGFLKWFALPFSLL	180
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DB	181	EFILPILVAVFSAHIYWSLMKREKLSRCLSHFVLPSDSSSDHGSCHRODPDSRATIPA	240
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DB	241	RKETTASLGSDDRKRKSSLLPSIRAYKNSNVIAIKMGFLSHSGLALQOEHEHLEPRARK	300

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DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21106319; PubMed=11179435;
RA Nguyen T., Shapiro D.A., George S.R., Setola V., Lee D.K., Cheng R.,
RA Rauber L., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RT "Discovery of a novel member of the histamine receptor family.";
RL Mol. Pharmacol. 59:427-433(2001).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
EMBL; AY008280; AAL09297.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR008102; Histamine_recept_H4.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0282; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane.
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Query Match 64.4%; Score 1310.5; DB 2; Length 390;
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Matches 253; Conservative 48; Mismatches 87; Indels 3; Gaps 3;
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DB 360 LCHKRFOKAFKILPVRQSTP-PHNSIST 389

RESULT 3
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DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Histamine H4 receptor (HH4R) (GPRV53) (G protein-coupled receptor 105)
DE (GPCR105) (SP9144) (AXOR35).
GN Name=HRH4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20538417; PubMed=10973974; DOI=10.1074/jbc.M006480200;
RA Oda T., Morikawa N., Saito Y., Masuno Y., Matsumoto S.-I.;
RT "Molecular cloning and characterization of a novel type of histamine
RT receptor preferentially expressed in leukocytes.";
RL J. Biol. Chem. 275:36781-36786(2000).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=leukocyte;
RX MEDLINE=20568725; PubMed=1118334; DOI=10.1006/birc.2000.4008;
RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
RT "Molecular cloning and characterization of a new human histamine
RT receptor, HH4R.";
RL Biochem. Biophys. Res. Commun. 279:615-620(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Jones P.G., Wu S., Betty M.;
RT "Cloning of a novel histamine receptor.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=bone marrow;
RX PubMed=11179434;
RA Liu C., Ma X.-J., Jiang X., Wilson S.J., Hofstra C.J., Blevitt J.,
RA Pyati J., Li X., Chai W., Carruthers N., Lovenberg T.W.;
RT "Cloning and pharmacological characterization of a fourth histamine
RT receptor (H4) expressed in bone marrow.";
RL Mol. Pharmacol. 59:420-426(2001).
RN [5]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=eosinophil;
RX MEDLINE=21106366; PubMed=11181941;
RA More K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A.,
RA Antles J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N.,
RA Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M.,
RA Monma F.J. Jr.;
RT "Cloning and characterization of a novel human histamine receptor.";
RL J. Pharmacol. Exp. Ther. 296:1058-1066(2001).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=21106320; PubMed=11179436;
RA Zhu Y., Michalevich D., Wu H.-L., Tan K.B., Dyck G.M., Mannan I.J.,
RA Boyce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L.,
RA Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S.,
RA Bergsma D.J., Fitzgerald L.R.;
RT "Cloning, expression, and pharmacological characterization of a novel
RT human histamine receptor.";
RL Mol. Pharmacol. 59:434-441(2001).
RN [7]
RP SEQUENCE FROM N.A.
RA O'Reilly M.A.;
RT "Identification of a histamine H4 receptor on human eosinophils - Role
```

RT in eosinophil chemotaxis." ;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Puhl H.L., Iikeda S.R., Aronstam R.S.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org)";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: The H4 subunit of histamine receptors could mediate the
 CC histamine signals in peripheral tissues. Displays a significant
 CC level of constitutive activity (spontaneous activity in the
 CC absence of agonist).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed primarily in the bone marrow and
 CC eosinophils. Shows preferential distribution in cells of
 CC immunological relevance such as T-cells, dendritic cells,
 CC monocytes, mast cells, neutrophils. Also expressed in a wide
 CC variety of peripheral tissues, including the heart, kidney, liver,
 CC lung, pancreas, skeletal muscle, prostate, small intestine,
 CC spleen, fetal liver and lymph node.
 CC -1- INDUCTION: Expression is either up-regulated or down-regulated
 CC upon activation of the lymphoid tissues and this regulation may
 CC depend on the presence of IL-10 or IL-13.
 CC -1- MISCELLANEOUS: Does not bind diphenhydramine, loratadine,
 CC ranitidine, cimetidine and chlorpheniramine. Shows modest affinity
 CC for dimaprit, imipramine, clobenpropit, thioferamide, burimamide
 CC clobazepam, imipipit and imetit. The order of inhibitory activity
 CC was imetit > clobenpropit > burimamide > thioferamide.
 CC Clobenpropit behaves as a partial agonist, dimaprit and
 CC imipramine show some agonist activity while clobazepam behaves as
 CC a full agonist. Thioferamide shows inverse agonism (enhances CAMP
 CC activity). The order of inhibitory activity of histamine
 CC derivatives was histamine > N-alpha-methylhistamine > R(-)-alpha-
 CC methylhistamine > S(+)-alpha-methylhistamine. Both N-alpha-
 CC methylhistamine > R(-)-alpha-methylhistamine behave as full
 CC agonists.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
 CC or send an email to license@1sb-sib.ch).
 CC -----
 DR EMBL; AB044934; BAB13698.1; -;
 DR EMBL; AB045370; BAB20091.1; -;
 DR EMBL; AF030793; AAG32052.1; -;
 DR EMBL; AF112330; AAK12081.1; -;
 DR EMBL; AF329449; AAK43542.1; -;
 DR EMBL; AF325356; AAL01684.1; -;
 DR EMBL; AJ298292; CAC83493.1; -;
 DR EMBL; AY136745; AAN01271.1; -;
 DR PIR; JC7566; JC7566;
 DR Genew; HGNC:17383; HRH4.
 DR MIM; 606792; -;
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0004569; F:histamine receptor activity; NAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR008102; Histamrecept_H4.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PRINTS; PR01726; HISTAMINHR4.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
 DR DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
 KM G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
 KM Transmembrane.
 FT DOMAIN 1 19 Extracellular (Potential).
 FT TRANSMEM 20 40 1 (Potential).
 FT DOMAIN 41 52 Cytoplasmic (Potential).
 FT TRANSMEM 53 73 2 (Potential).
 FT DOMAIN 74 87 Extracellular (Potential).

FT TRANSMEM 88 108 3 (Potential).
 FT DOMAIN 109 131 Cytoplasmic (Potential).
 FT TRANSMEM 132 152 4 (Potential).
 FT DOMAIN 153 172 Extracellular (Potential).
 FT TRANSMEM 173 193 5 (Potential).
 FT DOMAIN 194 304 Cytoplasmic (Potential).
 FT TRANSMEM 305 325 6 (Potential).
 FT DOMAIN 326 341 Extracellular (Potential).
 FT TRANSMEM 342 362 7 (Potential).
 FT DOMAIN 363 390 Cytoplasmic (Potential).
 FT DISULFID 87 164 By similarity.
 FT CARBOHYD 5 9 N-linked (GlcNAc...) (Potential).
 FT LIPID 374 374 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 138 138 S-palmitoyl cysteine (Potential).
 FT CONFLICT 206 206 H -> V (in Ref. 1).
 FT CONFLICT 253 253 H -> R (in Ref. 1).
 SQ SEQUENCE 390 AA; 44495 MW; C986B8AE7FE912C3 CRC64;
 Query Match 64.3%; Score 1308.5; DB 1; Length 390;
 Best Local Similarity 65.1%; Pred. No. 2,3e-80;
 Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;
 QY 5 NSTIALT-SIKISTFLMSLLAIAIMGNVVIATFVDRNLRHSNYFFLNIAIDFPV 63
 DB NSTINLSLSTRTVLAFPMGLVAFAIMGNALVILAFVVDKNLRHSYFFLNIAIDFPV 64
 QY 64 GAIAIPLIPSSLTITTSKQACVFELIDYLLCTSYNNIVILSDRQSVGNATWYRA 123
 DB GVISIPILYPHLTFEWDGEGELCVFWLTDYLLCTSYNNIVILSDRYSVSNAYSRT 124
 QY 124 QHSCTKIKITOMAVAVIFSPMTNGPMILISDSQNSTCEPFLKMYFALPTSLLEFL 183
 DB QHTGVAKITLWAVAVLAFVNGPMILVSESKDGSECEPFEWYIATTSLEFV 184
 QY 125 QHTGVAKITLWAVAVLAFVNGPMILVSESKDGSECEPFEWYIATTSLEFV 184
 QY 184 IPIILVAYFSAMITWYSLMKREKLSRCLSHPVLEPSDSSSDHGHSCQDDPSRATLPARKE 243
 DB IPVILVAYFNMNIYWSLMKRDHLRSCSHPLGLTA-VSSNICGHSFGRSLRSLSASTE 243
 QY 244 TTSLSDSKSRKSSLLPSTRAVKNVNIASKGFLSHSDSLAOREHTELPFRATLAK 303
 DB 244 VPSFSEQRKSSLMFSSRTKMTNSNTASKGSPSQSVALLHREHVELLRARLAK 303
 QY 304 SLAIIAALFAICAPASLTIVISFPERNLTKSTYHTAFWLOFNSFVNPLPLPLCHK 363
 DB 304 SLAIIIGVAVCAPASLTIVISFYSATGPASVYRIAFWLOFNSFVNPLPLPLCHK 363
 QY 364 RFOKAFKLILPVRRQSTP-PHNRSIST 389
 DB 364 RFOKAFKLIFCIKOPLPQSHRSVS 390
 RESULT 4
 ID Q912Y2 PRELIMINARY; PRT; 391 AA.
 AC Q912Y2;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, last sequence update)
 DE 01-OCT-2003 (T-EMBLrel. 25, last annotation update)
 GN Histamine H4 receptor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=BALB/C;
 RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF358859; AAK97380.1; -;

DR MGD; MGI:2429635; Hrh4.
 DR GO; GO:0005815; C:extracellular space; TAS.
 DR GO; GO:0005887; C:integral to plasma membrane; IC.
 DR GO; GO:0005624; C:membrane fraction; IDA.
 DR GO; GO:0004969; P:histamine receptor activity; IDA.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR01726; HISTAMINEH4R.
 DR PROSITE; PS00262; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 DR G-protein coupled receptor; Receptor; Transmembrane.
 KW G-PROTEIN COUPLED RECEPTOR; RECEPTOR; TRANSMEMBRANE.
 SQ SEQUENCE 391 AA; 44248 MW; 59EC73CB5214C5E0 CRC64;

Query Match 61.1%; Score 1244; DB 2; Length 391;
 Best Local Similarity 62.8%; Pred. No. 5, 1e-76;
 Matches 246; Conservative 43; Mismatches 99; Indels 4; Gaps 3;

QY 1 MANNSTGTLPPAAQVPLAFMSSFAFMVGNVAVIILAFVDRNLRRHSNYFFNLATA 59
 DB 1 MANNSTGTLPPAAQVPLAFMSSFAFMVGNVAVIILAFVDRNLRRHSNYFFNLATA 60
 QY 60 DEFVGAIAPIIYPSISLTWTSGKQACVFWLITDYLCTASVYNYVILSYDRYQSVNAV 119
 DB 61 DEFVGAISIPLYIPHYLFNMFSGICMFWLITDYLCTASVYNYVILSYDRYQSVNAV 120
 QY 120 WYRAHSGTWKATQWAVWIFSPMTNGPMILISDMONSTT--ECEPGFLKKWYFALPT 177
 DB 121 STRAGHTGIMKIVAQWVAVIILAFVNGMILASDMKSTTKCEPFEVWYIITTT 180
 QY 178 SLLEFLIPILVAVPSAHITWYSLWKREKLSRCLSHVLPSSSSSDHGHSCRODPSRAT 237
 DB 181 MLLEFLIPVISAAYEVNQIYWSLWKRRALSRCPSHAGF-STISSASGHLHAGVACRTS 239
 QY 238 LPARETTSLGSDSRKSSILPSIRAYKNSNYASKMGFLSHDSIALOOREHIEFLPARK 297
 DB 240 NGLESASASRHSSEPRKSSILVSRITMNSITAFKQSPWRSALRQREYAEILR 299
 QY 298 ARKLAKSLAILLAAPACWAPYSLTIVISFPERNLTKSTWYHTAFMLQWPNFSVNPPL 357
 DB 300 GRKLAKSLAILLSAPACWAPYCLFTIVSTYPRTRPSVWYSTAFMLQWPNFSVNPPL 359
 QY 358 YPLCHRFQKAFKLIPVRROSTPPHNSIST 389
 DB 360 YPLCHRFQKAFKILCVTKQPALSONGVSS 391

RESULT 5

Q91ZY1 PRELIMINARY; PRT; 391 AA.
 AC Q91ZY1;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
 DE Histamine H4 receptor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Liu C., Wilson S., Xuei C., Lovenberg T.W.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF358860; AAK97381.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.

DR PRINTS; PR01726; HISTAMINEH4R.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 391 AA; 44023 MW; C707BA6B39CFED41 CRC64;

Query Match 60.7%; Score 1235.5; DB 2; Length 391;
 Best Local Similarity 61.4%; Pred. No. 1, 9e-75;
 Matches 239; Conservative 46; Mismatches 101; Indels 3; Gaps 2;

QY 3 ANNSTIALTSIKISLTFLMSLATAIMGNVVIILAFVDRNLRRHSNYFFNLATAIDPF 62
 DB 4 SNGTDVLPRTQVPLAFMSSLAFAITTGNAVVIILAFVDRNLRRHSNYFFNLATISDF 63
 QY 63 VCAIPIPIYPSISLTWTSGKQACVFWLITDYLCTASVYNYVILSYDRYQSVNAWYR 122
 DB 64 VGVISIPLYIHTLFFNMFSGICMFWLITDYLCTASVYNYVILSYDRYQSVNAWYR 123
 QY 123 AOHSGTWKATQWAVWIFSPMTNGPMILISDMONSTT--ECEPGFLKKWYFALPTSL 180
 DB 124 AOHGTGILKIVAQWVAVIILAFVNGMILASDMKSTNTCECPFEVWYIITAFV 183
 QY 181 EFLIPILVAVPSAHITWYSLWKREKLSRCLSHVLPSSSSSDHGHSCRODPSRATPA 240
 DB 184 EFLIPVLSLVYFVSQIYWSLWKRGSLSRCPSHAGPIA-TSSRGTHSRRTGLACRTSLPG 242
 QY 241 RRETTASIGSDSRKSSILPSIRAYKNSNYASKMGFLSHDSIALOOREHIEFLPARK 300
 DB 243 LKEPAASLSHSEPRKSSILVSRITMNSGSIITAFVNGSFCRSSEVYLQREHVEILRRK 302
 QY 301 LAKSLAILLAAPACWAPYSLTIVISFPERNLTKSTWYHTAFMLQWPNFSVNPPL 360
 DB 303 LARSLAVILSAFACWAPYCLFTIVLSTYRGERPKSIWYSTAFMLQWPNFSLINFLVPL 362
 QY 361 CHKRFQKAFKLIPVRROSTPPHNSIST 389
 DB 363 CHKRFQKAFKILCVTKQPALSONGVSS 391

RESULT 6

Q8WNV9 PRELIMINARY; PRT; 390 AA.
 AC Q8WNV9;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
 DE Histamine H4 receptor.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22015261; PubMed=12020829; DOI=10.1016/S0167-4781(02)00236-1;
 RA Oda T., Matsunoto S., Masuno Y., Takasaki J., Matsunoto M., Kamohara M., Saito T., Ohishi T., Soga T., Hiyama H., Matsushime H., Furuchi K.;
 RT "cDNA cloning and characterization of porcine histamine H4 receptor."; Biochim. Biophys. Acta 1575:135-138(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AB053300; BAB83078.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR01726; HISTAMINEH4R.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.

SQ SEQUENCE 390 AA; 44483 MW; BCF8FD363A6F4D3F CRC64;
Query Match 60.0%; Score 1221.5; DB 2; Length 390;
Best Local Similarity 62.7%; Pred. No. 1.7e-74;
Matches 242; Conservative 45; Mismatches 92; Indels 11; Gaps 4;
QY 4 NNSTIALTSIKISLTFLMSLAIAIMGNVVIILAFVDRNLRHSNYPFLNLAIDPFV 63
DB 8 NNTPLPLNT-RIMLALFLMSLAIAVIMGNVVIILAFVDRNLRHSNYPFLNLAIDPFV 66
QY 64 GAIAIPLYIPSSITWTSGKQACVFWLITDYLLCTASVNIIVLISYDRYQSVNAWYRA 123
DB 67 GVISIPLYIPHTLFFKWKLEEDNICAFWLIIDYLLCTASVNIIVLISYDRYQSVNAWYRA 126
QY 124 QHSCTKINQWAVVIFSPMTGPMILISDSQNTTECEPEFLKMYAALFTSLLEFL 183
DB 127 QHTGIKIVLAWGVAVLAVHGPVILVSEAKQKQDEPEFLKMYAALFTSLLEFL 186
QY 184 IPIILVAFSAHIYMSLMKREKLSRCLSH---PVLPSDSSSDHGHSCRODPSRATLP 239
DB 187 APVLVAVYFNLYIYMSLMKRGHLSRCQSHGGLTPV-----SSGSMGHSRPGCLFSRTSL 241
QY 240 ARKETTASLGSDKSRKSSILPSIRAYKNSNVIASKMGFLSHSDSLAQREHIEFLRAR 299
DB 242 DPKEAASLSHSERPRKSTLMFSLRT-RMSLSLTAASKGFLSHSDSLALHKEHIELRAR 300
QY 300 KLAKSIALIILAAALICWAPISLTIVYSPFPEENLTKSTYHTAFWLQWNSVNFPLP 359
DB 301 KLAKSIALIILGVVAICWAPISLTITRSVYPTNPSTAYVKAFWLQWNSCVNPFLLP 360
QY 360 LCHKRFQKAFKILPVROSTPPHNSIST 369
DB 361 LCHKRFQKAFKILPVROSTPPHNSIST 390
RESULT 7
HH3R CAVPO STANDARD; PRT; 445 AA.
AC 09J135; 09J136;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Histamine H3 receptor (HH3R).
GN Name=HH3;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxId=10141;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RX TISSUE=Brain;
MEDLINE=20218440; PubMed=10757514;
RA Tardivel-Lacombe J., Rouleau A., Morisset S., Pillot C.,
RA Cochais V., Schwartz J.-C., Arrang J.-M.;
RT "Cloning and cerebral expression of the guinea pig histamine H3
RT receptor: evidence for two isoforms.";
RL NeuroReport 11:755-759(2000).
CC -1- FUNCTION: The H3 subclass of histamine receptors could mediate the
CC histamine signals in CNS and peripheral nervous system. Signals
CC through the inhibition of adenylyl cyclase and displays high
CC constitutive activity (spontaneous activity in the absence of
CC agonist).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long; Synonyms=H3L;
CC IsoId=09J135-1; Sequence=Displayed;
CC Name=Short; Synonyms=H3S;
CC IsoId=09J135-2; Sequence=VSP_001880;
CC -1- TISSUE SPECIFICITY: Expressed widely and abundantly throughout the
CC brain. Highly expressed in discrete neuronal populations such as
CC pyramidal cells in cerebral cortex or cerebellar Purkinje cells.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC -----
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CC or send an email to license@isb.ch).
CC -----
DR EMBL; AF267537; AAF78947.1; -;
DR EMBL; AF267538; AAF78950.1; -;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR003980; H3_Receptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PRINTS; PRO1471; HISTAMINEH3R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KM Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW Transmembrane.
FT DOMAIN 1 40 Extracellular (Potential).
FT TRANSMEM 41 61 Potential.
FT DOMAIN 62 71 Cytoplasmic (Potential).
FT TRANSMEM 72 92 Potential.
FT DOMAIN 93 109 Extracellular (Potential).
FT TRANSMEM 110 130 Potential.
FT DOMAIN 131 157 Cytoplasmic (Potential).
FT TRANSMEM 158 176 Potential.
FT DOMAIN 179 197 Extracellular (Potential).
FT TRANSMEM 198 218 Potential.
FT DOMAIN 219 359 Cytoplasmic (Potential).
FT TRANSMEM 360 380 Potential.
FT DOMAIN 381 398 Extracellular (Potential).
FT TRANSMEM 399 419 Potential.
FT DOMAIN 420 445 Cytoplasmic (Potential).
FT CARBOHYD 11 24 Poly-A1a.
FT DOMAIN 20 11 N-linked (GlcNAc...) (Potential).
FT VARSPIC 276 305 Missing (in isoform short).
SQ SEQUENCE 445 AA; 48734 MW; BAE206A5887189A0 CRC64;
Query Match 34.0%; Score 693; DB 1; Length 445;
Best Local Similarity 37.4%; Pred. No. 7.8e-39;
Matches 160; Conservative 67; Mismatches 139; Indels 62; Gaps 11;
QY 3 ANNSTIALTSIKISLTFLMSLAIAIMGNVVIILAFVDRNLRHSNYPFLNLAIDPFV 62
DB 27 ARTFSAATVAV---LAAALMALIVATVIGNALVMAFVADSSIRTONNFFLNLAIIDFL 83
QY 63 VGAIATPLTIPSLT-YMTSGKQACVFWLITDYLLCTASVNIIVLISYDRYQSVNAWY 121
DB 84 VGVFCIPLVPPVLTGRMTFGRLCLMLVVDLLCTSSVFNVLISYDRYQSVNAWY 143
QY 122 RAQHSCTKINQWAVVIFSPMTGPMILISDSQNTTECEPEFLKMYAALFTSLLEFL 174
DB 144 RAQGGTTRAVAKMVLVWLAFLVGPAL---SWVYLSGGSSIPRGCHCAEFYMWYFL 200
QY 175 LPTSLLEFLIPLILVAFSAHIYMSLMKREKLSRCLSHPVLPSSSS----- 221
DB 201 ITASTLEFFTPPLSFVFNLSIYLNIGRTTRRLDGAEEAGDPPLPEAQSSPPQPPPGC 260
QY 222 -----SDHGHSCRODPSRATLPARKETTASLGSDKSRK 256
DB 261 WGWCPKQGSBNPLHRYGVGEAGPGAEBAALAGGSGAASFTSSGSSSRCTEPR-- 318
QY 257 SSLPSIRAYKNSNVIASKMGFLSHSDSLAQREHIEFLRARLKAKSLAIIILAAFAICW 316
DB 319 -SLKRSKSSASASLEKMKWVQS-----ITQR--FRLSRDKVAKSLAIIIVSIGLCW 371
QY 317 APYSLTIVYSPFPEENLTKSTYHTAFWLQWNSVNFPLPCHKRFQKAFKILPV 376
DB 372 APYTLMIIRAC-HGHCVDPDYETSFWLWANSVNVNVLPLCHYSFRRAFTKLLCPQ 430

OY 377 ROSTEPHN 384
 :
 DB 431 KLVQPHS 438

 RESULT 8
 H3R_HUMAN STANDARD; PRT; 445 AA.
 AC Q9Y5N1; O9GZX2; O9H4K8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Histamine H3 receptor (H3R) (G protein-coupled receptor 97).
 GN Name=HRH3; Synonyms=GPR97;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxId=9606;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thalamus;
 RX MEDLINE=99279519; PubMed=10347254;
 RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
 RT Huvar A., Jackson M.R., Eriander M.G.;
 RT "Cloning and functional expression of the human histamine H3
 RT receptor.";
 RT Mol. Pharmacol. 55:1101-1107(1999).
 RN (2)
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
 RX MEDLINE=20568725; PubMed=1118334; DOI=10.1006/dbic.2000.4008;
 RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
 RT "Molecular cloning and characterization of a new human histamine
 RT receptor, HRH4.";
 RT Biochem. Biophys. Res. Commun. 279:615-620(2000).
 RN (3)
 RP SEQUENCE FROM N.A. (ISOFORMS 1, 3, 4, 5, 6 AND 7).
 RC TISSUE=Thalamus;
 RX MEDLINE=21181559; PubMed=11284713; DOI=10.1042/0264-6021.3550279;
 RA Cogde F., Guenlin S.-P., Audinat E., Renouard-Try A., Beauverger P.,
 RT Macia C., Ouvre C., Nagel N., Rigue H., Boutin J.A., Gallizi J.-P.;
 RT "Genomic organization and characterization of splice variants of the
 RT human histamine H3 receptor.";
 RT Biochem. J. 355:279-288(2001).
 RN (4)
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SHY-DRAGER SYNDROME
 VAL-280.
 RC TISSUE=Blood;
 RX MEDLINE=21953383; PubMed=11956964; DOI=10.1007/s007020200036;
 RA Wiedemann P., Boenisch H., Oerters F., Brunes M.;
 RT "Structure of the human histamine H3 receptor gene (HRH3) and
 RT identification of naturally occurring variations.";
 RT J. Neural Transm. 109:443-453(2002).
 RN (5)
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC Ulmer C., Zitzew E., Lubbert H.;
 RT "Cloning and functional expression of the human histamine H3
 RT receptor.";
 RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN (6)
 RP SEQUENCE FROM N.A. (ISOFORM 1)
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/41465a1;
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagunley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Gardner C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leivaeslatho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel A., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.F.,
 RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RT Nature 414:865-871(2001).
 CC -1- FUNCTION: The H3 subclass of histamine receptors could mediate the
 CC histamine signals in CNS and peripheral nervous system. Signals
 CC through the inhibition of adenylyl cyclase and displays high
 CC constitutive activity (spontaneous activity in the absence of
 CC agonist). Agonist stimulation of isoform 3 neither modified
 CC adenylyl cyclase activity nor induced intracellular calcium
 CC mobilization.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=Q9Y5N1-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9Y5N1-2; Sequence=VSP_001886;
 CC Name=3; Synonyms=H3S;
 CC IsoId=Q9Y5N1-3; Sequence=VSP_001885;
 CC Name=4;
 CC IsoId=Q9Y5N1-4; Sequence=VSP_001881;
 CC Name=5;
 CC IsoId=Q9Y5N1-5; Sequence=VSP_001882;
 CC Name=6;
 CC IsoId=Q9Y5N1-6; Sequence=VSP_001883;
 CC Name=7;
 CC IsoId=Q9Y5N1-7; Sequence=VSP_001884;
 CC -1- TISSUE SPECIFICITY: Expressed predominantly in the CNS, with the
 CC greatest expression in the thalamus and caudate nucleus. The
 CC various isoforms are mainly coexpressed in brain, but their
 CC relative expression level varies in a region-specific manner.
 CC Isoforms 3 and 7 are highly expressed in the thalamus, caudate
 CC nucleus and cerebellum while isoforms 5 and 6 show a poor
 CC expression. Isoforms 5 and 6 show a high expression in the
 CC amygdala, substantia nigra, cerebral cortex and hypothalamus.
 CC Isoform 7 is not found in hypothalamus or substantia nigra.
 CC -1- DISEASE: Defects in HRH3 are a cause of Shy-Drager syndrome
 CC [MIM:146500]. This syndrome is characterized by orthostatic
 CC hypotension, bladder and bowel incontinence, anhidrosis, iris
 CC atrophy, amyotrophy, ataxia, rigidity and tremor.
 CC -1- MISCELLANEOUS: Does not bind to cimetidine and triptolidine. Shows
 CC modest affinity for thioperamide, imetit, N-alpha-methylhistamine
 CC and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to
 CC idopropoxyfan while isoforms 1 and 3 bind it with high affinity.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
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 CC
 CC EMBL; AF140538; AAD38151.1; -
 CC EMBL; AB045369; BAB20090.1; -
 CC EMBL; AB019000; BAB17030.1; -
 CC EMBL; AJ296652; CACS1025.1; -
 CC EMBL; AJ278250; CAC39434.1; -
 CC EMBL; AL078633; CAC04014.1; -

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DR EMBL: AF363791; AAK50040.1; -.
DR Genew; HGNC:5184; HRH3.
DR MIM; 146500; -.
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0004969; F: histamine receptor activity; TAS.
DR GO; GO:0007187; P: G-protein signaling, coupled to cyclic nucl. .; TAS.
DR GO; GO:0007269; P: neurotransmitter secretion; TAS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR003980; H3_Receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
DR Alternative splicing; Disease mutation; G-protein coupled receptor;
KW Glycoprotein; Transmembrane.
FT DOMAIN 1 39
FT TRANSMEM 40 60
FT DOMAIN 61 70
FT TRANSMEM 71 91
FT DOMAIN 92 108
FT TRANSMEM 109 129
FT DOMAIN 130 156
FT TRANSMEM 157 177
FT DOMAIN 178 196
FT TRANSMEM 197 217
FT DOMAIN 218 359
FT TRANSMEM 360 380
FT DOMAIN 381 395
FT TRANSMEM 396 416
FT DOMAIN 417 445
FT DOMAIN 250 266
FT DOMAIN 292 298
FT CARBOHYD 11 11
FT VARSPLIC 85 98
FT VARSPLIC 197 315
FT VARSPLIC 227 342
FT VARSPLIC 234 263
FT VARSPLIC 274 353
FT VARSPLIC 445 445
FT VARIANT 280 280
FT CONFLICT 19 19
SQ SEQUENCE 445 AA; 48671 MW; 2ACF7440FBB95B6C CRC64;

Query Match 33.9%; Score 689.5; DB 1; Length 445;
Best Local Similarity 37.3%; Pred. No. 1.3e-48;
Matches 161; Conservative 70; Mismatches 132; Indels 69; Gaps 13;

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QY 223 -----DHGSHCRDPDSR-----ATL-----PARKETASIGSDK 252
DB 260 GCMQKHGEAM---PLHRYGVEAAGVAGEATLGGGGGGSVASPTSSGSSSNGTGR 316
QY 253 SRRKSSLPISRAYKSNVIAKMGFLSHSDSLAQORHIELFRARKLAKSLAIIIAAF 312
DB 317 PR---SLKRGSPKSPASASLEKRMKVQSFT-----ORFLRSRDRKVAKSLAVVSI 367
QY 313 AICMAPYSLTITVYSPFPERNLTKSTWHTAFTMLQWFSFVNPPLYPLCHKPQKAFKI 372
DB 368 GLCMAPYTLMLTIRAC-HGCVDPYWTSTFPLMANSAVNPVLPCLCHSFRRAFTYL 426
QY 373 LPVRRQSTPPHN 384
DB 427 LCPQKXIKQPHS 438

RESULT 9
ID 0865R1 PRELIMINARY; PRT; 445 AA.
AC 0865R1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Histamine receptor H3.
GN Name=HRH3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Yao B.B., Sharma R., Caesar S., Esbenshade T.A., Hancock A.A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AY231164; AAO63757.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004969; F: histamine receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR003980; H3_Receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PROSITE; PRO1471; HISTAMINEH3R.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 445 AA; 48591 MW; E79440A4EC09CA8C CRC64;

Query Match 33.8%; Score 688.5; DB 2; Length 445;
Best Local Similarity 37.8%; Pred. No. 1.6e-38;
Matches 161; Conservative 66; Mismatches 142; Indels 57; Gaps 12;

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QY	223	-----DHGSC---KODPSRSATLPARKET-----TSLGDK--SPRKS	252
Db	260	GCWGHGEMAMPLHRKYGVEAAGAAGETALGCGGCGGASPTSSGSSSNGTERPRS	319
QY	259	LLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFARKLAKSLATILAAFAICWAP	318
Db	320	LKRGSKPSSASASLEKRMKMGVSSQFT-----GRFLSDRKVAKSLAVIVSIFGLCMAP	373
QY	319	YSLTVIVSYFFPERNLTKSTWHTATWLOWFNSFVNPLPYPLCHKPQKAFKILPVRRQ	378
Db	374	YTLMIITRAAC-HGHCVPDPYWTYSFPLLMANSANVPVLPYLCHHSFRRAFTYLLCPQKL	432
QY	379	STPPHN 384	
Db	433	KIQPHS 438	
RESULT 10			
H3R RAT			
ID	H3R RAT	STANDARD:	PRT: 445 AA.
AC	09QYN8; 09QYNS; 09QYN7; 09QYN9;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Histamine H3 receptor (H3R).		
CN	Name=H3h3.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISU=Hypothalamus;		
RX	MEDLINE=2030707; PubMed=10869375;		
RA	Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;		
RT	"Cloning of rat histamine H3 receptor reveals distinct species		
RT	pharmacological profiles."		
RL	J. Pharmacol. Exp. Ther. 293:771-778(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).		
RC	TISU=Striatum;		
RX	MEDLINE=21016732; PubMed=11130725; DOI=10.1038/35048583;		
RA	Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J.,		
RA	Stark H., Schumack W., Ganelin C.R., Schwartz J.-C., Arrang J.-M.;		
RT	"High constitutive activity of native H3 receptors regulates histamine		
RT	neurons in brain."		
RL	Nature 408:860-864(2000).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1, 2, 3 AND 4).		
RA	Itadani H., Takimura T., Nakamura T., Ohta M.;		
RT	"Cloning of a novel G protein-coupled receptor."		
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBD databases.		
RN	[4]		
RP	TISU=SPECIFICITY.		
RX	MEDLINE=99278519; PubMed=10347254;		
RA	Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,		
RA	Huvar A., Jackson M.R., Erlander M.G.;		
RT	"Cloning and functional expression of the human histamine H3		
RT	receptor."		
RL	Mol. Pharmacol. 55:1101-1107(1999).		
CC	-1- FUNCTION: The H3 subclass of histamine receptors could mediate the		
CC	histamine signals in CNS and peripheral nervous system. Signals		
CC	through the inhibition of adenylylate cyclase and displays high		
CC	constitutive activity (spontaneous activity in the absence of		
CC	agonist).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=4;		
CC	Comment=Additional isoforms seem to exist;		
CC	Name=1; Synonyms=H3L;		
CC	Isoid=09QYN8-1; Sequence=Displayed;		
CC	Name=2; Synonyms=H3S;		
CC	Isoid=G9QYN8-2; Sequence=VSP_001887;		

CC	Name=3;
CC	Isoid=09QYN8-3; Sequence=VSP_001888;
CC	Name=1;
CC	Isoid=09QYN8-4; Sequence=VSP_001888, VSP_001889;
CC	TISSUE SPECIFICITY: Expressed abundantly in brain, most notably
CC	throughout the thalamus, the ventromedial hypothalamus and the
CC	caduate nucleus. Isoform 1 is largely predominant in all tissues.
CC	-MISCLEANEONS: Proxylan acts as a potent neutral antagonist while
CC	thioperoxamide, ciprofloxan and FUD465 act as potent inverse
CC	agonists.
CC	-I SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC	-----
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CC	-----
DR	EMBL; AF237919; AAF82086.1; -
DR	EMBL; AY009370; AAK02069.1; -
DR	EMBL; AB015646; BAA88765.1; -
DR	EMBL; AB015646; BAA88766.1; -
DR	EMBL; AB015646; BAA88767.1; -
DR	EMBL; AB015646; BAA88768.1; -
DR	RCD; 620630; Hrh3.
DR	InterPro; IPR000276; GPCR_Rhodopsn.
DR	InterPro; IPR003980; H3_receptor.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRHOPOPSN.
DR	PRINTS; PR01471; HISTAMINEH3R.
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR	PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KM	Alternative splicing; G-protein coupled receptor; Glycoprotein;
KM	Transmembrane.
FT	DOMAIN 1 39
FT	TRANSMEM 40 60
FT	DOMAIN 61 70
FT	TRANSMEM 71 91
FT	DOMAIN 92 108
FT	TRANSMEM 109 129
FT	DOMAIN 130 156
FT	TRANSMEM 157 177
FT	DOMAIN 178 196
FT	TRANSMEM 197 217
FT	DOMAIN 218 359
FT	TRANSMEM 360 380
FT	DOMAIN 381 396
FT	TRANSMEM 397 417
FT	DOMAIN 418 445
FT	DOMAIN 445 23
FT	CARBOHYD 11 11
FT	VARSPPLIC 274 305
FT	Missing (in isoform 2).
FT	/ftid=VSP_001887.
FT	Missing (in isoform 3 and isoform 4).
FT	/ftid=VSP_001888.
FT	VARSPPLIC 393 445
FT	Missing (in isoform 4).
FT	/ftid=VSP_001889.
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FT	/ftid=VSP_001887.
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FT	/ftid=VSP_001888.
FT	VARSPPLIC 393 445
FT	Missing (in isoform 4).
FT	/ftid=VSP_001889.
FT	Missing (in isoform 2).
FT	/ftid=VSP_001887.
FT	Missing (in isoform 3 and isoform 4).
FT	/ftid=VSP_001888.
FT	VARSPPLIC 393 445
FT	Missing (in isoform 4).
FT	/ftid=VSP_001889.
FT	Missing (in isoform 2).
FT	/ftid=VSP_001887.
FT	Missing (in isoform 3 and isoform 4).
FT	/ftid=VSP_001888.
FT	VARSPPLIC 393 445
FT	Missing (in isoform 4).
FT	/ftid=VSP_001889.
FT	Missing (in isoform 2).
FT	/ftid=VSP_001887.
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FT	/ftid=VSP_001888.
FT	VARSPPLIC 393 445
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FT	/ftid=VSP_001889.
FT	Missing (in isoform 2).
FT	/ftid=VSP_001887.
FT	Missing (in isoform 3 and isoform 4).
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FT	/ftid=VSP_001889.
FT	Missing (in isoform 2).
FT	/ftid=VSP_001887.
FT	Missing (in isoform 3 and isoform 4).
FT	/ftid=VSP_001888.
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FT	Missing (in isoform 4).
FT	/ftid=VSP_001889.
FT	Missing (in isoform 2).
FT	/ftid=VSP_001887.
FT	Missing (in isoform 3 and isoform 4).
FT	/ftid=VSP_001888.
FT	VARSPPLIC 393 445
FT	Missing (in isoform 4).
FT	/ftid=VSP_001889.
FT	Missing (in isoform 2).
FT	/ftid=VSP_001887.
FT	Missing (in isoform 3 and isoform 4).
FT	/ftid=VSP_001888.
FT	VARSPPLIC 393 445
FT	Missing (in isoform 4).
FT	/ftid=VSP_001889.
FT	Missing (in isoform 2).
FT	/ftid=VSP_001887.
FT	Missing (in isoform 3 and isoform 4).
FT	/ftid=VSP_001888.
FT	VARSPPLIC 393 445
FT	Missing (in isoform 4).
FT	/ftid=VSP_001889.
FT	Missing (in isoform 2).
FT	/ftid=VSP_001887.
FT	Missing (in isoform 3 and isoform 4).
FT	/ftid=VSP_001888.
FT	VARSPPLIC 393 445
FT	Missing (in isoform 4).
FT	/ftid=VSP_001889.
FT	Missing (in isoform 2).
FT	/ftid=VSP_001887.
FT	Missing (in isoform 3 and isoform 4).
FT	/ftid=VSP_001888.
FT	VARSPPLIC 393 445
FT	Missing (in isoform 4).
FT	/ftid=VSP_001889.
FT	Missing (in isoform 2).
FT	/ftid=VSP_001887.
FT	Missing (in isoform 3 and isoform 4).
FT	

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Oy      63  GGAIAIPYIPESLS- YMTSGQACAFMLITDYLCITASVYVILSYORVOSVANAWY 121
Db      83  VGAFICILPLYVYVLGRMTFGRLCKLMLVDDLCASSVFNVLISYDFELSVTRAVSY 142
Oy      122  RAQHSGTAKIAQOMYAWMIFSEFMTPGMLILSDSWO-----NSTTE--CEPGELKKMYFA 174
Db      143  RAQGDGDTRAVAKMALVWLAFLVLGPAL--SWYILGGSSILPEGHCAEFYMYWYFL 199
Oy      175  LPTSLLEFLPILLVAVYSAHIYWSIMKEKL--SRCLSHPVLPDSGSSS----- 222
Db      200  ITASTLEFETPPLSTVFFMLSTIYLIQRTRLRLDGRAGPEPPDAGSPPPAPPSCW 259
Oy      223  -----DHGHSQCDPDNR-----ATLPARETTASIGSDK 252
Db      260  GCWPKGHEAM--PLHRYGVGEAGPVEAGEALGSGSGGGAAPSTSSGSSRGCTER 316
Oy      253  SRRKSSLLPPIRAYKNSVNIASKMGLSHSDSLALQOREHIELFPRAKLAKSLATILAA 312
Db      317  PR---SLKRGSKFPAASALEKRMKVSSG---ITQR--FLRSRDKYAKSLAIIIVSIF 367
Oy      313  AICWAPYSLLTVIYSEFFPERNLTKSTWYHTAFWLOFNSFVNDFLYPLCHKRPQKAFLE 372
Db      368  GLCWAPYLLMTIIRAAHGRCI-PDYWEYETSFWLLWANSVNVNVLPLCHYSFRRAPFTKL 426
Oy      373  LPVRRQSTPRH 383
Db      427  LCPQRLKVPQH 437

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RESULT 11			
HH3R_MOUSE	STANDARD:	PRT:	445 AA.
ID_HH3R_MOUSE			
AC	P56406;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Histamine H3 receptor (HH3R).		
GN	Name=Hh3;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CD-1;		
RA	Cocq F., Rigue H., Levecher B., Leopold O., Guenin S.-P., Boutin J.A.,		
RA	Galizzi J.-P.;		
RT	"Cloning of mouse histamine H3 receptor.";		
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: The H3 subclases of histamine receptors could mediate the		
CC	histamine signals in CNS and peripheral nervous system. Signals		
CC	through the inhibition of adenylyl cyclase and displays high		
CC	constitutive activity (spontaneous activity in the absence of		
CC	agonist) (By similarity).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AY044153; AAK72406.1; -		
DR	MCD; MG1:2139279; Hrh3.		
DR	InterPro; IPR000376; GPCR_Rhodopsn.		
DR	InterPro; IPR003980; H3_receptor.		
DR	Pfam; PF00001; 7cm1.1		
DR	PRINTS; PR00237; GPCRHHODOPSN.		
DR	PRINTS; PR01471; HISTAMINEH3R.		
DR	PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.		

DR	PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
KM	G-protein coupled receptor; Glycoprotein; Transmembrane.
FT	DOMAIN 1 39 Extracellular (Potential).
FT	TRANSSEM 40 60 Potential.
FT	DOMAIN 61 70 Cytoplasmic (Potential).
FT	TRANSSEM 71 91 Potential.
FT	DOMAIN 92 108 Extracellular (Potential).
FT	TRANSSEM 109 129 Potential.
FT	DOMAIN 130 156 Cytoplasmic (Potential).
FT	TRANSSEM 157 177 Potential.
FT	DOMAIN 178 196 Extracellular (Potential).
FT	TRANSSEM 197 217 Potential.
FT	DOMAIN 218 359 Cytoplasmic (Potential).
FT	TRANSSEM 360 380 Potential.
FT	DOMAIN 381 396 Extracellular (Potential).
FT	TRANSSEM 397 417 Potential.
FT	DOMAIN 418 445 Cytoplasmic (Potential).
FT	DOMAIN 20 23 Poly-Ala.
FT	CARBOHYD 11 11 N-linked (GLCNAC...) (Potential).
SQ	SEQUENCE . 445 AA; 48541 MW; B8D06E29E1F3CSF CRC64;
Query Match	33.4%; Score 679.5; DB 1; Length 445;
Best Local Similarity	37.4%; Pred. No. 6,4e-38;
Matches 161; Conservative 65; Mismatches 136; Indels 69; Gaps 13	

Qy	3	ANNSTIALTSIKISLTFELMSLLAIAMIGNVVLLAFIVDNLBHRSNYPFLNLAIADPF	62
Db	26	ARGSSAAMTAV---LALMLALIYATVLGNALLVWLAFVADSLSTLQNNFLLNLAIADPFL	82
Qy	63	VGAIALIPLYPSSLT-YWTSKQACVFMLITDYLLCTASVTNIVLISIDRYQSVSNAAWY	121
Db	83	VGAFICILYVPYVLTGRWTFGRGLCKLMLVDVLLICASSVENIVLISYDRFLSVTRAVSY	142
Qy	122	RAOHSGMTKATATQWVAWVWISFPMTNGPMLISDSMO-----NSTTE--CEBGFLLKWVEA	174
Db	143	RAOQGDTRRAVRKRALVWLAFLLYGAAIL---SWEIYISGSSSIPEGCIAFEFLNMYFL	199
Qy	175	LPTSLLEFLIPLILVAYFSAHYIWSLWKREKL---SRCLSHPVLPSSDSSS-----	222
Db	200	ITASTLEFFPEFLSVTFEPNLISLYNIQRTRLRLDGGREAGPEPPPDQAPPPAPPCW	259
Qy	223	-----DHGSGROQDPDSR-----ATLPARKTTASLGSDK	252
Db	260	GCMWKGGEAAR--PLHRYGVGEAGPEVETGEAGLGGSGGGAASPSSSGSSSRGTER	316
Qy	253	SRRSKSLPIRSIRAYKSNVLIASKMGFLSDPSLALQOREHIEFLRARKLAKSLAILLAAFL	312
Db	317	PR---SLKRGSKPEASSASLEKMKWVSQSG---ITQR--FLRLRDKVVAASLAIIVSIF	367
Qy	313	AICAAPISLTTVVISFPPERNLTSTYHTAFWLQWFNSFNPPLPYLPLCHKRFQKAFKI	372
Db	368	GLCAAPATLLMIIPAAC-HGHCVDPDYETSFMLIMANSANVPLVPLCHXSFRAATKL	426
Qy	373	LPVNRQSTPPH 383	
Db	427	LCFQKLKVGPH 437	
RESULT 12			
Q6ZM33	PRELIMINARY;	PRT,	473 AA.
AC	Q6ZM33;		
DT	05-JUL-2004 (TREMBLrel. 27, Created)		
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
DE	SI.b234G2.4 (Novel protein similar to human histamine receptor H3 (HRH3)).		
GN	Name=si:rp71.34G2.4; Synonyms=SI.b234G2.4;		
OS	Brachydanio rerio (Zebrafish) (Danio rerio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
CC	Cyprinidae; Danio.		
NCBI	TaxID=7955;		

RN [1]
 RP SEQUENCE FROM N.A.
 RA Tracey A.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBS databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL: AL928906; CAFE49238.1; -;
 DR ZFIN: ZDB-GENE-040724-204; sl:fp71-3492.4.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0004969; F:histamine receptor activity; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PRINTS: PR01471; HISTAMINEH3R.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Receptor; Transmembrane.
 SK SEQUENCE 473 AA; 53506 MW; 032RC7C27D8C6B57 CRC64;

Query Match 32.7%; Score 666; DB 2; Length 473;
 Best Local Similarity 37.5%; Pred. No. 5.5e-37;
 Matches 155; Conservative 64; Mismatches 148; Indels 46; Gaps 12;

QY 12 SIKISLTFMSLALAIAMGNVVIAPFVDRNLHRSNVFFLNLAIDPFVGAIAIPY 71
 DB 62 STSIFLVTMTLVATVGNALVILAFVVEKSLRQGNFFLNLAIDFLVGGCIPY 121
 QY 72 IPSSLT-YWTSGKQACVFWLITDYLLCTASVYNIIVISYDRYQSVNNAVYPAQHSQTWK 130
 DB 122 IYVVLTEGRLRGLCKMLVVDYMLCTASVFNIVLISFDRFQSVTKAVSYRCQKITD 181
 QY 131 IATQVAVVIFPMNGMFWILISDSQNST-----TCEPGLKKWFAIPSLILETL 183
 DB 182 AVLKMLCWLAAFLVYGPAIL--SWEHLTGSGVVPDGCYAEFFNWYFLMTASTVERF 238
 QY 184 IPILVAYSAHIYMSLMREKLS-----RCLSHPVLPSSSSSDHSGCRQDPDSR- 235
 DB 239 TFFISVTYNNLSITINIRRCAMREQPTVYVLRSLKMKPLGAGDVQRTFPRVPEBSIV 298
 QY 236 ATLPAKRE-----TTSAL-----GSDKSRKRSLSL-PSIRAYKNSNVIA--SKMGF 278
 DB 239 ADLARSRCRLSTAKVSAAEFGNGRQGRDSTLADPLQV--EERILLASEAQPHY 356
 QY 279 LSHS-----DSLALQREHTELPRARKLAKSLALLAFAICWAPYSLTIVISFPPE 331
 DB 357 VDHSAQPHRRPDMVASLANRFLSRDKVAKSLAVICVFGLCWAPYLLMIIRAAC-H 415
 QY 332 RLUTSTWYHTAFWLQWFNFSFVNPFLYPLCHKRFOKAFKILPVRROSTPPHN 384
 DB 416 GGCYGHVLYEISFWLIMINSINPILYPLCHSSFKRAFSKLCPSKTKIQPON 468

RESULT 13

Q8WY01 PRELIMINARY; PRT; 365 AA.
 AC Q8WY01;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Histamine H3 receptor isoform 2.
 GN Name=HRH3;
 OS Homo sapiens (Human).
 CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN NCB1_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RA Wellendorp P., Goodman M.W., Birstein E.S., Nash N.R., Brann M.R.,

RA Weiner D.M.;
 RT "Molecular Cloning and Characterization of Functionally Distinct
 RT Isoforms of the Human Histamine H3 Receptor."
 RL Neuropharmacology 0:0-0(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL: AF321911; AAL71912.1; -;
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0004969; F:histamine receptor activity; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PRINTS: PR01471; HISTAMINEH3R.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Receptor; Transmembrane.
 SK SEQUENCE 365 AA; 40609 MW; D7BB32042464CB35 CRC64;

Query Match 32.2%; Score 655.5; DB 2; Length 365;
 Best Local Similarity 36.7%; Pred. No. 2.2e-36;
 Matches 146; Conservative 60; Mismatches 111; Indels 81; Gaps 10;

QY 3 ANNSTIALTSIKISLTFMSLALAIAMGNVVIAPFVDRNLHRSNVFFLNLAIDPF 62
 DB 26 ARGFSAMTAV---LAALMALIVATVGNALVILAFVADSLSLRQNNFFLNLAISDFL 82
 QY 63 VGAIAPILYIPSSLT-YWTSGKQACVFWLITDYLLCTASVYNIIVISYDRYQSVNNAVY 121
 DB 83 VGAFCLPILVFPVYLVGRMTFGRLCKMLVVDYLLCTASAFIVLISDRFLSVRAVS 142
 QY 122 RAQHSQTKIATQVAVVIFPMNGMFWILISDSQNST-----NSTTE--CEPGLKKWFA 174
 DB 143 RAQQGDTRAVRKMLVWVLAFLVGPAIL--SWEYLSGSGSIIEGCVAEFFNWYFL 199
 QY 175 LPTSLILEFLIPLLVAYSAHIYMSLMREKLS-----SKLSHPVLPSSSSSDHSG---H 226
 DB 200 ITASTLBEFTFPPLSTFPNLSTYINIQRTTRRLDGAEEAGPEPPPEQAPPPPPCGW 259
 QY 227 SCRODPDSRATLPARKETTAGLSGDSKSRKSSLSIRAYKNSNVIAAGWGLSHSDSLA 286
 DB 260 GCMQR-----GHGEANP 271
 QY 287 LQOREHIELFARKLAKSLALLAFAICWAPYSLTIVISFPFRNLTKSTWYHTAFWL 346
 DB 272 LH-----RKVAKSLAVIVSIFGLCWAAPYLLMIIRAAC-HGHCVPDYWYERSFWL 320
 QY 347 QWFNFSFVNPFLYPLCHKRFOKAFKILPVRROSTPPHN 384
 DB 321 LWANSAVNPVYPLCHHSFRRAFTLCPQKLIKIQPHS 358

RESULT 14

Q8WXZ9 PRELIMINARY; PRT; 373 AA.
 AC Q8WXZ9;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Histamine H3 receptor isoform 4.
 GN Name=HRH3;
 OS Homo sapiens (Human).
 CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN NCB1_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RA Wellendorp P., Goodman M.W., Birstein E.S., Nash N.R., Brann M.R.,
 RA Weiner D.M.;
 RT "Molecular Cloning and Characterization of Functionally Distinct
 RT Isoforms of the Human Histamine H3 Receptor.";

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RL Neuropharmacology 0:0-0(2002).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AF321913; AAL7914.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004969; F:histamine receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR Pfam: PF00001; Tm 1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 373 AA; 41570 MW; FAEEDFCSCAFDE9 CRC64;

Query Match 32.2%; Score 655.5; DB 2; Length 373;
Best Local Similarity 36.7%; Pred. No. 2.2e-36;
Matches 146; Conservative 60; Mismatches 111; Indels 81; Gaps 10;

QY 3 ANNSTALSIKISLFLKSLAIAIMLVVLAIFIDRNLRHSNYEFLNLATADFF 62
DB 26 AAGFSAMTAV--LALMALIIVATVLSNALVMLFVADSSLRQNNFFLNLAISDFL 82
QY 63 VCAIAPLYIPESLT-YMTSGQACVFWLITDYLCTASVYNIIVLISYRQSVSNVAVY 121
DB 83 VQAFCEPLVPLVLTGRWTFGRGLCKLWLVVDLICTSSAFNIVLISYRFLSVTRAVSY 142
QY 122 RAQHGSTMATQWAVAVMTFSMTNGPMILISDSWC---NSTTE-CEPGFLKKWYRA 174
DB 143 RAQCGTTRAVAKMLVWLAFLYGPAIL---SWEYLSGSSIPGHCYAEFFYMWYFL 199
QY 175 LPTSLLEFLPLLVAVFSAHYWSLMKREKL---SRCLSHPVLPSSSSSDHG---H 226
DB 200 ITASTLEFTPLSVTFEFLSYILNIQRKTRLLDGAARADAGEPPEPAOPSPPPPGCW 259
QY 227 SCROPDPSRATLPARKETTASLGSDDRKRSLSLPSIRAYKSNVYASKMGFLSHDSIA 286
DB 260 GCMQK-----GHGEAMP 271
QY 287 LOQREHIELFARKKLAKSLAIIILAFATCMAPYSTTVIYSPFERNLTKSTWYHTAFWL 346
DB 272 LH-----RKVAKSLAVIVSIFGLCMAPYTLIMIRAC-HGHCVPDYWYETSPWL 320
QY 347 QWFNSFVNPLYLCHKRFQKAFKLTPRRROSTPPHN 384
DB 321 IMAVSAVNPVLYPLCHHSFRFAFTKLLCPQKLIQPHS 358

RESULT 15
ID 06J9J4 PRELIMINARY; PRT; 174 AA.
AC 06J9J4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Histamine receptor H4 subtype (Fragment).
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15123584; DOI=10.1101/gr.1891104;
RA Zhang J., Wang X., Podlana O.;
RT "Testing the chromosomal speciation hypothesis for humans and
RT chimpanzees."
RL Genome Res. 14:845-851(2004).
DR EMBL: AY561470; NAT4508.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.

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DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR Rhodpsn.
DR InterPro: IPR008102; Histamine_recept_H4.
DR Pfam: PF00001; Tm 1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PRINTS: PR01726; HISTAMINE4R.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
FT NON TER 1 1
FT NON TER 174 174
SQ SEQUENCE 174 AA; 19713 MW; 4038B74734A785F5 CRC64;

Query Match 26.3%; Score 534.5; DB 2; Length 174;
Best Local Similarity 62.4%; Pred. No. 1.5e-28;
Matches 108; Conservative 18; Mismatches 46; Indels 1; Gaps 1;

QY 206 LSRCLSHPVLPSSSSSDHGCGRQDPDSRATLPARKETTASLGSDDRKRSLSLPSIRA 265
DB 2 LSRCSHPGL-TGVSSNLCGHSPFRGLSSRSLSASAEVPASLHSERRQRKSLMPSRST 60
QY 266 YKNSNVIASKMGFLSHDSIALQOREHIELFARKKLAKSLAIIILAFATCMAPYSTTVI 325
DB 61 KMSNSTIAKMGFSQSDSVLHOREHVELLARKRLAKSLAIIILGVFAVCMAPYSTTVI 120
QY 326 YSFFPERNLTKSTWYHTAFWLQWFNSFVNPLYLCHKRFQKAFKLTPRRRO 378
DB 121 LSFYSATGPKSVMYRIAFWLQWFNSFVNPLYLCHKRFQKAFKLTPRRRO 173

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Search completed: August 3, 2005, 01:57:01
Job time : 174 secs

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